GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

May 26, 2004, 15:20:44 ; Search time 417.308 Seconds (without alignments) 3115.905 Million cell updates/sec Run on:

US-10-676-299-3 Title: Perfect score:

1 ttaatcatatgcgtttttggttatgtgttg 30 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 3.0 Scoring table:

6940544 Total number of hits satisfying chosen parameters:

3470272 segs, 21671516995 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmb1:\* Database :

1: gb ba:\*
2: gb htg:\*
3: gb n:\*
4: gb om:\*
6: gb pat:\*
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14: gb vi:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

	ECRFARSR	B. coli R-fac	X16045	X16045.1 GI:	arsenical res
RESULT 1 ECRFARSR	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS

ALEVAS.1 GI:42716 arsR gene; ArsR protein; DNA-binding protein; Escherichia coli Bacherichia coli Bacherichia coli Bacherichia coli Bacherichia coli

REPERENCE AUTHORS

SOURCE ORGANISM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

In (bases 1 to 727)

San Francisco, M.J., Hope, C.L., Owolabi, J.B., Tisa, L.S. and Rosen, B.P.

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Mutational analysis of the R64 oriT region: requirement for precise location of the Nika-binding sequence J. Bacteriol. 179 (23), 7291-7297 (1997) 98053841
                                                                                                                                                                                                                                                                                                                                           Furuya, N. and Komano, T. Determination of the nick site at oriT of IncIl plasmid R64: global similarity of oriT structures of IncIl and IncP plasmids J. Bacteriol. 173 {20}, 6612-6617 {1991}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshida,T., Furuya,N., Ishikura,M., Isobe,T., Haino-Fukushima,K., Ogawa,T. and Komano,T.

Purification and characterization of thin pili of Incil plasmids Colli-P9 and R64: formation of PilV-specific cell aggregates by type IV pili

J. Bacteriol. 180 (11), 2842-2848 (1998)
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Nuclectide sequence and characterization of the traABCD region of
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J. Bacteriol. 178 (6), 1491-1497 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Furuya, N. and Komano, T. Suria and Rota incleding sequence saclusion gene of IncII plasmid R64: nuclectide sequence and analysis of deletion mutants plasmid 32 (1), 80-84 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Narahara,K., Rahman,E., Furuya,N. and Komano,T.
Requirement of a limited segment of the sog gene for plasmid R64
conjugation
Plasmid 38 (1), 1-11 (1997)
97428559
                                                                        and Nisioka, T.
the oriT region of the Incll
                                                                                                                                                                                                         Furuya, N., Nisioka, T. and Komano, T. Nucleotide sequence and functions of the oriT operon in Incil plasmid R64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The plasmid R64 thin pilus identified as a type IV pilus J. Bacteriol. 179 (11), 3594-3603 (1997) 97315231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IncIl plasmid R64
J. Bacteriol. 175 (16), 5035-5042 (1993)
                                                                                                                 J. Bacteriol. 170 (9), 4385-4387 (1988)
88314948
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213 (1), 30-35 (1988)
                                                       Komano, T., Toyoshima, A., Morita, K.
Cloning and nucleotide sequence of plasmid R64
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Salmonella typhimurium plasmid R64 DNA, complete sequence.
AP005147
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Mucleotide sequence of the rci gene encoding shufflon-specific DNA recombinase in the Incli plasmid R64: homology to the site-specific recombinases of integrase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="unnamed protein product; ArsR protein (AA 1 - 117)"
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Submitted (09-AUG-1989) Rosen B.P., Department of Biochemistry,
Wayne State University, School of Medicine, 54- B Canfield Avenue,
Detroit MI 48201, U.S.A.
Location/Qualifiers
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Salmonella typhimurium
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Enterobacteriaceae; Salmonella.
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Shufflon: multi-inversion of four contiguous DNA segments
plasmid R64 creates seven different open reading frames
Nucleic Acids Res. 15 (3), 1165-1172 (1987)
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Identification of the metalloregulatory element of the plasmid-encoded arsenical resistance operon Wholeic Acids Res. 18 (3), 619-624 (1990)
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Cardenas, V., Carter, K., Cavacos, I., Ceasar, H., Center, A.,
Clacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Coyle, M., Cree, A., D'Souza, L.,
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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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location 3593. .3597 and location 20833. .20837 are
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Rattus norvegicus clone CH230-296C3, WORKING DRAFT SEQUENCE.
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HTG: HTGS_PHASR2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus
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join (3542. .3597,20833. .22533)
/nore="arsA"
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                                                                                                                                                                                                                                                                                                                                                                                                        codon start=1
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3162. .3524
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29; Conservative
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Best Local
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HPPYVQKRTFVGRKYAFRPEKORLLDAIWPVLVSFSDAGTHTVGMSVTRLAEEISPKD
SEGHVIPELEVTVSRLSRLLAEQVRPGVLGVSEETMWDREHRQRLPRYWITPAGWQM
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REKAAASKRANRLKKLPVDQQIYEMAEYLRKRLPPDBEAYFCSDDHLKRLAIRELRQLE
LTLAAPPPH"
                                                                                                                                                                                                                                                                                                                                                                          Sampei, G., Komano, T., Sasaki, T., Tachibana, K., Furuya, N., Saito, Y., Suzuki, T. and Mizobuchi, K.
Organization and diversification of plasmid genomes: complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xomano,T., Sasaki,T., Tachibana,K., Furuya,N., Saito,Y., Suzuki,T.,
Sampei,G. and Mizobuchi,K.
Direct Submission
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                                                                                                                           Komano,T., Yoshida,T., Narahara,K. and Furuya,N.
The transfer region of IncIl plasmid R64: similarities between R64
The tra and legionella icm/dot genes
Mol. Microbiol. 35 (6), 1348-1359 (2000)
20223621
10760136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-MAY-2002) Gen-ichi Sampei, The University of Electro-Communications, Applied Physics and Chemistry; Chofugaoka 1-5-1, Chofu, Tokyo 182-8585, Japan (E-mail:sampei@pc.uec.ac.jp, Tel:81-42-44-43-541, Fax:81-424-43-5501)
Location/Qualifiers
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/codon start=1
/trans1_table=11
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'gene="repz"

/roce="100 pct identical to sp:REPZ_ECOLI, sp:P18023 [Repz

of plasmid Collb-P9]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (join (2004). 20418, 3609. .4147))
/note="100 pot identical to sp:YI22_ECOLI[hypothetical protein of insertion sequence IS2]
location complement (4143. .4147) and location complement (20047. .20051) are dupulicated"
378. .467
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/mol type="genomic DNA"
/mol trype="taxon:602"
/lab host="Escherichia coli strain K-12"
/plasmid="R64"
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'protein id="BAB91567.1"
'db_xref="G1:20521503"
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/protein_id="BAB91568.1"
/db_xref="G1:20521504"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequence of R64 genome
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transl_table=
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/gene="repy"
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/gene="repz"
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/gene="arsR"
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Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Havlak, P., Hadun, S.L., Hodgson, A., Hogues, M., Hollins, B., Houlins, F., Hulyk, S., Hum, J., Idlebird, D., Jackson, L., Jackson, L., Jackson, L., Jackson, E., Hulyk, S., Khan, Z., King, L., Govar, C., Karfar, C.L., Lebow, H., Johnson, B., Johnson, R., Jolivet, A., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liz, T., Liu, M., Liu, W., Liu, Y., Londseged, H., Lordacre, S., Lopez, J., Lorensuhewai, M., Mallindartne, M., Mahnoud, M., Malloy, K., Martin, R., Martin, R., Martin, R., Martin, R., Mangum, A., Mangum, B., Magua, P., Martin, R., Morris, S., Munidasa, M., Murphy, M., Nair, L., Navackelemeh, O., Okwuon, G., Okunon, G., Primus, E., Pu, L.-L., Parter, M., Minidasa, M., Murphy, M., Nair, L., Parter, A., Pender, S., Punk, H., Perez, L., Primus, E., Pu, L.-L., Priopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Priopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Priopper, F., Poindexter, A., Rechin, R., Reeves, K., Regier, M., Sakelly, M., Sall, 
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Direct Submission

Worley.K.C.

Submitted (14-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23856412.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.Mgsc.bcm.tmc.edu/projects/rat/). Each config described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are crdered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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Center clone name: GT30-296C3
Center clone name: GT30-296C3
Assembly program: Phrap; version 0.990329
Consensus quality: 172459 bases at least Q30
Consensus quality: 173621 bases at least Q30
Consensus quality: 174370 bases at least Q20
Estimated insert size: 177946; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
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2 (bases 1 to 177109)
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COMMENT

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RE MIZIN, D. Marie, Metzer, M. Lee., Abramzon, S., Adams, C., Alder, J., C., C., Marie, Metzer, M. Lee., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayogi, M., Baca, E., Baden, H., Balanbechi, V., Bandaranaike, D., Barber, M., Barnstead, M., Benamed, F., Biswalo, K., Blair, J., Blarch, P., Burrell, K., Calderon, B., Cardenas, V., Carter, K., Cavacos, I., Ceasar, H., Center, A., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Clavelanai, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., Disouca, D., Davila, M. L., Davila, M. D., Davila, M. L., Davila, M. D., Davila, M. L., Davila, M. D., Denson, S., Deramo, C., Coyle, M., Cree, A., Dioya, K., Egan, A., Escotto, M., Eugene, C., Evens, C., Poyle, M., Flaggi, N., Fotbes, L., Foster, M., Gebregeorgis, E., Geer, K., Galli, R., Gardy, M., Guerra, M., Gurerra, W., Guerra, M., Gunerra, W., Harlandez, S., Finley, M., Hawes, A., Handlon, C., Hamilton, C., Mangue, M., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, M., Liu, W., Liu, W., Loudon, P., Lowan, J., Lewis, L., Liu, J., Liu, M., Liu, W., Loudon, P., Lowan, J., Lowis, C., Lopez, J., Liu, M., Liu, W., Liu, W., Mahnoud, M., Malloy, K., Mangum, A., Liu, W., Mahnidartne, M., Mahmoud, M., Malloy, K., Mangum, A., Liu, W., Mahnidartne, M., Mahmoud, M., Malloy, K., Mangum, M.,
                                                              NOTE: Betimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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***, 6 unordered pieces.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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HTG, HTGS_PHASEL; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
| mol rype="genomic DNA"
| db xref="taxon:10116"
| clone="CH230-29663"
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77.3%; Score 23.2; D
Best Local Similarity 89.3%; Pred. No. 64;
Matches 25; Conservative 0; Mismatches
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/note="wgs_contig"
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Homo sapiens chromosome 3 clone RP11-7B12, complete sequence. AC099326 AC010957 AC099326.1 GI:16874860 HTG.
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Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2 (Dasses 1 to 152772)
2 (Dasses 1 to 152772)
KAULR.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
Submitted (09-NOV-2001) Genome Center, University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (24-JAN-2002) Genome Center, University of Washington,
Submitted (24-JAN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Nov 9, 2010 this sequence version replaced gi:10198411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Box 352145, Seattle, WA 98195, USA
3 (bases I to 152772)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
      * This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.3%; Score 23.2; DB 2; Length 199985; 89.3%; Pred. No. 63;
                                                                                           170190: contig of 170190 bp in length 170290: gap of unknown length 190268: contig of 22678 bp in length 190368: gap of unknown length 19488: contig of 1420 bp in length 194588: gap of unknown length 195684: contig of 1096 bp in length 195784: gap of unknown length 197789: contig of 1096 bp in length 197769: contig of 1086 bp in length 197269: gap of unknown length 197269: contig of 2716 bp in length
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Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
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Center clone name: RP11-7B12 (bc0603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"

| mol Lype="genomic DNA"

| db xref="taxon:10116"

| clone="CH230-42116"
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170291. .172609
/note="wgs_contig"
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Best Local Similarity
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TITLE
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3 {bases 1 to 199983}

S Rat Genome Sequencing Consortium.

Direct Submission

Bylor Diaza Houston, TX 77030, USA

Direct Submission

Nolecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:25009137.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bom.tmc.edu/projects/fart). Each config described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence ends. Both end sequences and whole genome shotgun sequence ends. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, B.,
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Weinstock, G. and Gibbs, R.A.
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NOTE: This is a 'working draft' sequence. It currently consists of a contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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Worley, K.C.
Direct Submission
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REFERENCE AUTHORS TITLE JOURNAL

TITLE

TITLE JOURNAL

COMMENT

REPERENCE AUTHORS

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Gaps

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3; Indels

5231 5077 2323 2348 650 <800 2843 2906 1357 1309 13741 13713 5157 5077 5192 5120 60 <800	181 <800 10560 10611 5778 6013 1636 1608 758 <800 2421 2399	556 <800 10106 10165 1491 1472	1494 1474 5709 5695 2486 2399	360 <800 342 <800 1861 1904	2762 12854 1	638 <800 1893 1917 16 <800	<800	<pre>&lt;800 3190 3256 1286</pre>	6477 2488 2541 3630 3895	414 <800 5865 5695 1037 1057	1457 1442	5628 5695	756 <800 496 <800 6587 6827	5394 5422 886 979 2148 2160	1063 1053 4473 4390 10135 10124	1128	3606 3376 465 <800 719 <800	4911 5077 7137 7196 2175 2160	208 <800 1039 979 2	5151 5077 234 <800 1064 1057	918 923 4265 4216 3648 3895	4060 4080 934 979 10740 10687	6 <800 6627 6519 2316 2399	3376 1468 1442 3583 3433	675 <800 2168 2121 2782 2789	707 <800 951 979 188 <800	1393 2380 2339 2439 319 <800	8957 8700 2842 2869	3442 3662 3748 3728	4672 4584 1164 1128	2212 2288 3610 3585	4156 4080 3583 3585
Sequencing vector: plasmid; 34% of reads Sequencing vector: unknown; 66% of reads Chemistry: Dye-terminator ET: 57% of reads Chemistry: Dye-terminator EI by Dye; 47% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 152669 bases at least Q40	Consensus quality: 154792 bases at least 030 Consensus quality: 152772 bases at least 020 Insert size: 152772; sum-of-contigs Quality coverage: 11.0x in 020 bases; sum-of-contigs	Overlapping Sequences:		Sequence Quality Assessment:	estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero.	s above 40 are expected to have less than 0.000 bp.	Base-by base quality values are not generally visible from the Genbank flat file format but are available as part	of this entry's ASN.1 file.	This sequence was finished as follows unless otherwise noted:	alternate chemistry or covered by high high data (i.e., Phred	quality >= 30/; a: accempt was made to resolve all sequencing problems; such as compressions and repeats; all regions were	subclone; and the assembly was confirmed by restriction digest.	Sequence Validation:	This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest	iragments with sequence-predicted iragments is given below. The electronically-digested sequence consists of both insert and	vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp)	are not resolved in the inderprint and hence do not appear in the table. There are no significant remaining discrepancies	Detwen ine experimental ana predicted values, uniquery ordered fragments are separated by dashed lines.	THE PROPERTY OF A PROPERTY OF	sequermap rigiriic sequermap	8 K 9 K 9 K 9 K 9 K 9 K 9 K 9 K 9 K 9 K	7900 0134 C825 0000	2547 512 5800 8527	3178 449 4800 1335	5077 FELL 8077	2547 2746 2762 4253 4	1005 Tru0 235	1300 1501 1501 1501 1501 1501 1501 1501	1000 CF07 CF07 OCF7	3682 3783 2893 3662 3956 3889 16122 1	2000 976 9786	8159 5364 5343 3498

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/organism="Homo sapiens"
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Numberted (28-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, WA 02141, USA

On Mar 8, 2000 this sequence version replaced gi:6978150.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens clone RP11-7D10, WORKING DRAFT SEQUENCE, 25 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177672)
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Center code: WIBR
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Pred. No. 1.9e+02;
0; Mismatches 5; Indels 0
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<800
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HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 83.3%;
Matches 25; Conservative
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NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Center clone name: 7_D_10

Sequencing vector: M13, M79815, 100% of reads
Sequencing vector: M13, M79815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 1849787 bases at least Q30
Consensus quality: 162330 bases at least Q30
Consensus quality: 162331 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 182000; agarose-fp
Insert size: 187272; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1129; contig of 1129 bp in length 2465; gap of 100 bp 2410; contig of 1645 bp in length 4110; contig of 100 bp 7711; gap of 100 bp 7712; gap of 100 bp 7712; gap of 100 bp 7713; gap of 10
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183748)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-JAN-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA.

5 (bases 1 to 183748)

Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z., Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-UNN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
3 (Dases 1 to 183748)
3 (Dases 1 to 183748)
5 (Dases 1 to 183748)
6 (Dases 1 to 183748)
6 (Dases 1 to 183748)
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                                                                                                                                                                                                                                                                                                           2 (bases 1 to 183748)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
AC124915
AC124915.5 GI:30061451
                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                      Haugen, B.D.
Direct Submission
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Direct Submission
                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                       Unpublished
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file. Overlapping Sequences: 5': RP11-444P10 (UWGC:bc0656) AC104445, 107092-bp overlap 3': RP11-7B12 (UWGC:bc0603) AC099326, 76535-bp overlap Sequence Quality Assessment:

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Gaps

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PRI 23-APR-2003

AC124915 183748 bp DNA linear PRI 23-APP Homo sapiens chromosome 3 clone RP11-717N7, complete sequence.

RESULT 7 AC124915 LOCUS DEFINITION

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quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest

increases is given below. sists of both insert and the entire circular BAC. farmonymetaly 400.800 bm)	discrepancies	III	FngrPrnt	096	6430	<800	<800	6430	<800	506	4397	1175	<800	7195	096	<800	4397	907	9969	1463	2156	096	2321	2826	3687	1175	3533	3533	<800
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4129	4110	6624	6581	7339	7195
683	<800	719	< 800	655	×800
345	<800	857	884	1883	1886
342	<800	1592	1570		8784
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1647	1608	8423	8403	1963	2015
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2549	2589	22	2241	4581	4397
i	1065	9	9619	24	<800
632	<800	20	2038	1	4653
3489	3588		6849	;	8331
4	<800			2573	2641
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38	3798			i	<800
363	<800			2262	2321
1023	1065			2642	2641
Query Match Best Local Similarity 83. Matches 25; Conservative	73.3%; 83.3%; rative	Score 22; DB Pred. No. 1.8 O; Mismatches	9; e+02;	Length 183748; ; Indels 0;	Gaps
1 TTAATCATA	GCGTTTTT		30		
141399 TTAATCATCT	GTGTATTT		141428		
RESULT 8 AC108840/C LOCUS AC108840 DEFINITION Mus musculus	clone RE	207683 bp clone RP23-34897, WOR	DNA 15 WORKING DRAFT	near HTG SEQUENCE,	22-OCT-2002 11 ordered
ACCESSION AC108840. VERSION AC108840.3 GI:24211310 XEYWORDS HTG; HTGS PHASE2; HTGS_DRAFT; H7 SOURCE Mus musculus (house mouse)	GI:242113 AASE2; HTC s (house n	110 SS_DRAFT; HTGS nouse)	HTGS_FULLTOP.		
RGANISM Mus musculus Eukaryota; M	s fetazoa; (	Chordata; Cran	Craniata, Ver	Vertebrata; Buteleostomi	eleostomi;

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Insert size: 206683; sum-of-contigs
Quality coverage: 10.0 in Q20 bases; agarose-fp
Quality coverage: 10.2 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submitted (313-502) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA (Bases 1 to 207683)

E 3 (Bases 1 to 207683)

E 3 (Bases 1 to 207683)

E 4 (Bases 1 to 207683)

E 5 (Barren, B., Nusbaum, C., Jander, E., Ali, A., Allen, N., Anderson, S., Barran, B., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farreiza, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matria, V. M., Maclin, J., Moneus, L., Mihova, T., Matria, V., Murphy, T., Naylor, J., Mander, E., Major, J., Malora, V., Murphy, T., Naylor, J., Mander, C., Naicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Rise, C., Rogov, P., Roman, J., Roy, Schauer, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Mwman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Submitted (122-007-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 22, 2002 this sequence version replaced gi:20303870.

All repeats were identified using RepeatMasker: html
Center code: Wile Research
Center: Whitehead Institute/MIT Center for Genome Center Center Center code: Wile Research
Center: Whitehead Institute/MIT Center for Genome Center Center Code: Wile Research
Center: Whitehead Institute/MIT Center for Genome Center Center Code: Wile Research
    Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 207683)
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------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 20690 bases at least Q40
Consensus quality: 206544 bases at least Q30
Consensus quality: 206664 bases at least Q30
Insert size: 210000; agarose-fp
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                                                                                   Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-348P7
                                    REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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JOURNAL
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AUTHORS
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Gaps
NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs, days between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                          by the finished sequence as soon as it is available and the accession number will be preserved.

2554
2653: gap of 100 bp
2654
3493: contig of 840 bp in length
3494
5599: contig of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189852: contig of 48016 bp in length
189952: gap of 100 bp
207683: contig of 17731 bp in length.
                                                                                                                                                                                                                                                                                                                                                                100 bp
of 63271 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
of 32827 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                      114754: contig of 32827 bp in length
114854: gap of 100 bp
141736: contig of 26882 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
of 48016 bp in length
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                                                                                                                                                                                                                                                      100 bp
of 1941 bp in length
                                                                                                                                                                                                                                                                                                            of 2504 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                             of 8342 bp in length
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83.3%; Pred. No. 1.8e+02;
ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                          100 bp
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1594. .5369
note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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|hote="assembly_fragment"
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/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 2553
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189953. .2076837
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L. .207683
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol type="genomic DNA"
/db xref="taxon:10090"
/clone="RP23-348P7"
/clone_lib="RPCI-23 Fem
                                                                                                                                                                                                                                                      gap of J
                                                                                                                                                                                                                                                                                                            contig
gap of 1
contig
                                                                                                                                                                                                                                                                                                                                                    contig
gap of 1
contig
gap of 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
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vector_side:left"
2654. .3493
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Conservative
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HTG 20-OCT-2003 7 unordered

SOURCE ORGANISM

ACCESSION VERSION REFERENCE AUTHORS TITLE

COMMENT

RESULT 9 BX248100/c DEFINITION

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Submitted (18-OCT-2003) Wellcome Trust Sanger Institute, Hinxton, cambridgeshire, CB10 18A, UK. B-mail enquizites: zfish-help@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk on Oct 20, 2003 this sequence version replaced gi:36916794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 295094)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 291016 bases at least Q40
Consensus quality: 29920 bases at least Q30
Consensus quality: 29951 bases at least Q30
Insert size: 294494; sum-of-contigs
Insert size: 268382; 6.2% error; agarose-fp
Quality coverage: 15.71x in Q20 bases; sum-of-contigs Quality
coverage: 17.30x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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6: gap of 100 bp
2: contig of 13716 bp in length
2: optig of 100 bp
8: contig of 22246 bp in length
8: gap of 100 bp
8: gap of 100 bp
                                                                                                                                                                                                                              BX649429 295094 bp DNA linear Danio rerio clone DKEY-1H4, WORKING DRAFT SEQUENCE,
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35300: gap of 100 bp
70426: contig of 35126 bp in length
70526: gap of 100 bp
52836: contig of 82310 bp in length
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Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Wellcome Trust Sanger Institute
Center code: SC
                                                             62379 TTAATCATATGCTTTTTTTTTTTTTTTTG 62350
                           1 TIMATCATATGCGTTTTTGGTTGTTG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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1. .35200
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                                                                                                                                                                                                                                                                                                                                          BX649429.3 GI:37776961
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166753
188999
189099
236931
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                                                                                                                                                                                                                                                                                                                 BX649429
                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                      RESULT 10
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

EM:, EMBL: Sw:, SMISSPROT: Tr:, TREMBL: WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/brojects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononcleoride A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.
                                                                                                                                                                                                  BX248100 223-JUL-2003
Zebrafish DNA sequence from clone CH211-222011 in linkage group 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (22-707-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: Zish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 22, 2003_this sequence version replaced gi:32168874.
                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Grafilopterygli, Neopeerygli, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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CH211-222011 is from a CHORI-211 BAC library
VBCTOR: pTARBAC2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 1.8e+02;
0; Mismatches 5; Indels 0
                        123931 TTAATCATGTGTGTTTAATTATGTGTTG 123902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute
TTAATCATAIGCGTTTTIGGTTAIGTGTTG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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/clone="CH211-222011"
/clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Genome Center
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                                                                                                                                                                                                                                                                                                                                                                           Danio rerio (zebrafish)
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Watches 25; Conservative
                                                                                                                                                                                                                                                            complete sequence
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Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Nelson, K.E., Bisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F., Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, B.K., Haft, D.H., Salzberg, S.L., White, O., Pieischmann, R.D., Cougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, B., Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H., Pizza, M., Candi, G.J., Sanl, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappuoli, R. and Venter, J.G.
Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8
Science 287 (5459), 1809-1815 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
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Neisseria meningitidis MC58
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
1 (bases 1 to 10099)
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Diagnosis of diseases associated with dna transcription
Patent: WO 0192565-A 11 06-DEC-2001;
Epigenomics AG (DE)
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Human DNA sequence from clone RP11-341B24 on chromosome 10, Complete sequence.
ALS13533
ALS13533.15 GI:21213137
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KVEEDGKKLIIDELLTERSRKLGGGVPGAGGKYSMHIYDFYLPEGBYLPEISDNSEYI
SIGSFYLLNLLWIIWCLMIHREQVPLNNLTLLLSPIPSLFFLLCDFVLLLNVYVYFFK
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Submitted (23-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 18A, UK. F-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:20338446.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                               /note="similar to GB:L06302 PID:150255 SP:P55126 percent identity: 77.78; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148151)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7240. .7779
/gene="NMB1410"
/note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:X59756 percent identity: 84.00; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%; Score 21.6; DB 1; Length 10099; 85.7%; Pred. No. 4e+02; ive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transI_table=11
/produce="1S1016C2 transposase"
/protein id="AAR4173.1"
/db_xref="GI:7226649"
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complement (7950. .8603)
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                                      /gene="NMB1409"
/g575. .7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      table=11
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/gene="NMB1410"
                                                                                                                        575. .7003
gene="NMB1409"
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/transl_table=1
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Best Local Similarity 85...
Local 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        putative"
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SOURCE
ORGANISM
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AL513533/c
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VERSION
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AUTHORS
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                                                                                                                                                                                                                                                                /codon_start=1
/transT_table=11
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/producE="PrpA/c-related_protein"
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/db_xref="G1:7226644"
/db_xre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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/protein.id="AAR41763.1"
/db_xref="G1:722645"
/translation="WARSLEPRCOXIYFIVFILFICLYLNISYDGRIPIYFIINFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="This region contains a gene with one or more
premature stops or frameshifts, and is not the result of a
sequencing arrifact; similar to GB:106302 PID:150255
SP:P55126 percent identity: 92.67; identified by sequence
                      /trānslation="MIGSGDTKQCKKFSACDGKYHVYDPLALDLDGDGIETVTAKGFS
GSLKTERVNTMSIHSMPLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSLFDHNGNGIRTATGWVSADDGLLVRDLNGNGIIDNGAELFGDNTKLADGSFAKHGY
AALAELDSNGDNIINAADAAFQSLRVWQDLNQDGISQANFLRTLEELGIQSLDLAYKD
VNKNLGNGNTLAQQGSYTKTDGTFAKMGDLLLAADNLHSRFTNKMLSISHVRENTISP
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nylsilliyllelicsiymfifficktkdtitterrkkffnsifplrilmiigsbkkrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:106302 PID:150255 SP:P55126 percent
identity: 93.58; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein; identified by Glimmer2; putative"
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                                                                                                                                                                                                  /note="hypothetical protein; identified by Glimmer2; putative"
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/protein_id="AAF41770.1"
/db_xref="GI:7226646"
'db_xref="GI:7413467"
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5953. .6447
/gene="NMB1408"
5953. .6447
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/gene="NMB1405"
2756. .3958
/gene="NMB1405"
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/gene="NMB1406"
4389. .4751
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                                                                                          2014. .2742
/gene="NMB1404"
                                                                                                                                              2014. .2742
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/gene="NMB1407"
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/gene="NMB1408"
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AC144801 174303 bp DNA linear ROD 04-DEC-2003
Mus musculus chromosome 18 clone RP24-276M2, complete sequence.
AC144801
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 174303)
        Chemistry: Dye-terminator; 100% of reads
Consensus quality: 167966 bases at least Q40
Consensus quality: 168229 bases at least Q30
Consensus quality: 168484 bases at least Q20
Insert size: 165213; sum-of-contigs
Insert size: 170871; 31% error; agarose-fp
Quality coverage: 8.69x in Q20 bases; sum-of-contigs Quality
coverage: 8.68x in Q20 bases; agarose-fp
                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary, days between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.0%; Score 21.6; DB 2; Length 169613; Best Local Similarity 85.7%; Pred. No. 2.6e+02; Matches 24; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1167 4266. gap of 100 bp

1267 27503: contig of 23237 bp in length

1267 27603: gap of 100 bp

12604 27603: gap of 100 bp

12606 85775: gap of 100 bp

12606 85775: gap of 100 bp

12606 88719: gap of 100 bp

12607 88719: gap of 100 bp
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fragment_Chain:I"
85776. .88619
/note="assembly_fragment:00679"
88720. .169613
/note="assembly_fragment:00756.0"
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fragment_chain:1"
1267..27503
/note="assembly_fragment:01353
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="DanioKeypilot"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of Mus musculus clone Unpublished
2 (bases 1 to 174303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .169613
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-46C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AATCATAIGCGTTTTTGGTTAIGTGTG 30
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27504
27604
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885776
88620
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LOCUS
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ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
REFERENCE
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation amy not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by a least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMED: Sw.; SWISSPROT; Tr., TERBEL; Wp.; WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 http://www.sanger.ac.uk/HGP/Chr10
RPII-341B24 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chozie.c.uk/HGP/Chr10
PRII-341B24 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chozie.c.uk/HGP/Chr10
PRII-Decation/Qualifiers
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Direct Submission

Cambridgeshire, (26-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, Candon ISA, UK. E-mail enquiries:

zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Cn Jul 1, 2003 this sequence version replaced gi:29603281.

Center: Wellcome Trust Sanger Institute

Center code: SC
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etcinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 169613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%; Score 21.6; DB 9; Length 148151; 85.7%; Pred, No. 2.7e+02;
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BX321886.5 GI:32398460
HTG, HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62859 TAATAATAGGGGGGTTTGGTTTTCTGTT 62832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
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/chromosome="10"
/clone="RP11:341B24"
/clone_lib="RPCI-11:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TAATCATATGCGTTTTTGGTTATGTGTT 29
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Matches 24; Conserv
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Gaps

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Wilson,R.K.

Direct Submission

Submitted (20-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Submitted (20-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Johases I to 174303)
Wilson,R.K.

Direct Submission
Submitted (40-DEC-2003) Genome Sequencing Center, 4444 Forest Park
Darkway, St. Louis, MO 63108, USA
On Dec 4, 2003 this sequence version replaced gi:30911155.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                       Query Match 72.0%; Score 21.6; DB 10; Length 174303; Best Local Similarity 85.7%; Pred. No. 2.6e+02; Matches 24; Conservative 0; Mismatches 4; Indels 0;
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Source
 AUTHORS
TITLE
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                                                        REFERENCE
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8 6

Search completed: May 26, 2004, 17:21:57 Job time: 425.308 secs

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GenCore version 5.1.6
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	Copyright (c) 1993 - 2004 Compugen Ltd.
OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	May 26, 2004, 15:20:44 ; Search time 389.487 Seconds (without alignments) 3115.905 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-676-299-4 / 28 1 caacacataaccaaaaacqcatatqatt 28
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Database :	GenEmbl:*

em\_sy:\* em\_htgo\_htm:\* em\_htgo\_mus:\* em\_htgo\_other:\* em\_sts:\*
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em\_trg\_hum:\*
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em\_htg\_other:\*
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em\_htg\_pln:\*
em\_htg\_rod:\*
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gb htg:\*
gb ba:\*
gb pa:\*
gb pa 

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB ID  26.4 94.3 120626 1 AP005147  21.2 77.1 162613 2 BCRFARRR X16645 E.  21.2 77.1 162613 2 AC030562  21.2 77.1 163013 10 ACC44801  21.2 75.7 174303 10 ACC44803  22.0 73.6 166762 2 ACC13294  22.0 73.6 166762 2 ACC13294  23.6 218580 6 ACC42676  24.0 73.6 166762 2 ACC13294  25.0 72.1 151930 0 CCS6286  26.0 73.6 166762 2 ACC13294  27.1 181902 2 ACC13294  27.1 181902 2 ACC13294  27.1 181902 2 ACC12574  27.1 161903 2 ACC12574  27.1 161904 2 ACC12574  27.1 161908 2 ACC12574  27.1 161904 2 ACC12574  27.1 161908 2 ACC12574  27.1 161904 2 ACC12574  27.1 1619	No.							
1 28 100.0 727 1 ECRFARSR AND		Score	Match	Length	DB	Ω.	Descripti	uo
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5 21.2 75.7 73000 2 ACCOSO552  5 21.2 75.7 73000 2 ACCOSO552  9 21.2 75.7 174303 10 AC144801  9 21.2 75.7 174303 10 AC144801  9 21.2 75.7 174303 10 AC144801  2 21.2 75.7 174303 10 AC144801  2 21.2 75.7 174303 10 AC144801  2 21.2 75.7 174303 10 AC130151  2 20.6 73.6 6391 6 AXCO32523 ACCO30156  13 20.6 73.6 65842 9 ACC091766  14 20.6 73.6 16985 10 AL928957  15 20.6 73.6 16985 10 AL928957  16 20.6 73.6 16985 10 AL928957  2 20.6 73.6 16985 10 AL928957  2 20.6 73.6 16982 2 AC122166  2 20.6 73.6 16982 2 AC132163  2 20.6 73.6 16982 2 AC13213  2 20.6 73.6 16982 2 AC130303  2 20.2 72.1 189902 2 AC130303  3 2 20.2 72.1 189902 2 AC130303  4 1 10.3 10 10 10 10 10 10 10 10 10 10 10 10 10		21.6		w		AC007638	80 (	
5 21.2 75.7 164811 9 ACC20553 ACC20519 ACC2052 ACC20519 ACC2052 ACC20519 ACC2052 ACC20		21.2				AC090562	700	HOMO Sapi
21.2   75.7   177109   2 ACT18161.     21.2   75.7   177109   2 ACT18161.     21.2   75.7   184897   9 ACC39019   ACC301919     21.2   75.7   184897   9 ACC39019   ACC301919     20.6   73.6   10099   1 AB002489   ACC301766     20.6   73.6   10099   1 AB002489   ACC301766     20.6   73.6   10099   1 AB002489   ACC301766     20.6   73.6   10099   1 AB002489   ACC31766     20.6   73.6   100127   2 ACC32166   ACC32166     20.6   73.6   100127   2 ACC32166   ACC32166     20.6   73.6   100127   2 ACC32166   ACC32166     20.6   73.6   100127   2 ACC3885   ACC368977   ACC68977     20.6   73.6   2007674   8 ATTCAR   ATTCAR   ACC68977     20.6   73.6   2007674   8 ATTCAR   ACC68977   ACC68977     20.6   73.6   2007674   8 ATTCAR   ACC68977   ACC68977     20.6   73.6   2007674   BATTCAR   ACC68977   ACC68978     20.2   72.1   151990   ACC32913   ACC32913   ACC32913     20.2   72.1   181902   ACC32686   ACC32913   ACC32913   ACC32913     20.2   72.1   224453   2 ACC33686   ACC32913   ACC32913     20.2   72.1   20066   2 ACC32673   ACC32913   ACC32913     20.2   72.1   20066   2 ACC32673   ACC32913   ACC32913     20.2   72.1   20066   2 ACC32913   ACC32913   ACC32913     20.2   72.1   ACC3686   ACC32686   ACC32913   ACC32913   ACC32913     20.2   72.1   ACC3913   ACC32913   ACC32913   ACC32913     20.2   72.1   ACC3913   ACC32913		21.2						200
10   21.2   75.7   184697   9   ACC0501919   10   21.2   75.7   184697   9   ACC0501919   ACC0	- a	4. 4. 6			2		AC118161	2016
10 21.2 75.7 199985 2 ACI30151 ACI30151 ACI30151 20.6 73.6 65942 9 AC091766 AC091767	oo	21.2				AC090919	AC090919	Š
11 20.6 73.6 6391 6 AX23523 AX33523 AX33523 BEOCA489 DECOCA689 ACCOUTAGE BEOCA489 DECOCA689 ACCOUTAGE BEOCA689 ACCOUTAGE BEOCA689 ACCOUTAGE BEOCA689 ACCOUTAGE BEOCA689 ACCOUTAGE BEOCA689 ACCOUTAGE BEOCA689 ACCOUTAGE BEOCA6897 BEOCA68977 BEOCA6977 BEOC	m	21.2				AC130151		Rattus no
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13 20.6 73.6 65542 9 AC091766 AC091766 AC091766 1 14 20.6 73.6 110685 10 AL928957 AC122166 AC022166 AC072166 1 15 20.6 73.6 148151 9 AL913533 AC1568977 AC152166 AC058852 1 19 20.6 73.6 169178 AC068977 AC06877 AC068977 AC06897	12	20.6		10099		AB002489	_	Neisseria
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17 20.6 73.6 160127 2 AC068977 AC068977 AC068977 2 Co.6 73.6 166762 2 AC065852 AC065850 AC065852 AC06886 AC068897 AC068897 AC06886	16	20.6				AL513533	AL513533	Human DNA
18 20.6 73.6 166762 2 ACOSS852 ACOSS852 20 6 73.6 198788 8 ATCHRIV46 AL161546 20 6 73.6 217584 2 ACI12299 ACL13299 21 20.6 73.6 217584 2 ACI12299 ACL13299 22 20.6 73.6 218580 6 AXC440927 ACC440927 23 20.6 73.6 218580 6 AXC440927 ACC440927 24 20.2 72.1 151345 2 ACI32213 ACI322913 25 20.2 72.1 181904 2 ACI32213 ACI322913 27 20.2 72.1 181902 2 ACC32286 ACC32286 28 20.2 72.1 181902 2 ACC32286 ACC32286 29 20.2 72.1 181902 2 ACI32283 ACI132913 30 20.2 72.1 224453 2 ACI32283 ACI13293 31 20.2 72.1 224453 2 ACI32283 ACI13293 32 20.2 72.1 224453 2 ACI32283 ACI13293 33 20.2 72.1 22485 2 ACI32283 ACI13293 34 20 71.4 1553 6 ACC25734 ACC25734 ACC25734 35 20 71.4 1553 6 ACC25734 ACC25734 ACC25734 36 20 71.4 12787 1 AE015654 ACI226453 37 20 71.4 12787 1 AE015654 ACI226453 38 20 71.4 108582 2 ACI22469 ACI226459 41 20 71.4 131805 2 ACI32488 ACI38846 42 20 71.4 131805 2 ACI32488 ACI38846 43 20 71.4 131805 2 ACI38846 ACI38846 44 20 71.4 131805 2 ACI38846 ACI38846 45 20 71.4 131805 2 ACI38846 ACI38846 47 20 71.4 131805 2 ACI38846 ACI38846 47 20 71.4 131805 2 ACI38846 ACI38846 48 20 71.4 131805 2 ACI38846 ACI38846 49 20 71.4 131805 2 ACI38846 ACI38846 40 20 71.4 131805 2 ACI38846 ACI38846 41 20 71.4 131805 2 ACI38846 42 20 71.4 131805 2 ACI38846 ACI38846 43 20 71.4 131805 2 ACI38846 ACI38846	**1	20.6				AC068977	AC068977	Homo sapi
19         20.6         73.6         198788         B         ATCHRIV46         AL161546           20         20.6         73.6         20784         B         ATCHRIV46         AC11329           21         20.6         73.6         218580         2         AC14027         AC140927         AC140927           22         20.6         73.6         218580         2         AC140927         AC140927           24         20.2         72.1         151930         2         AC140927         ACC1440927           25         20.2         72.1         151930         2         AC13603         AC13603           26         20.2         72.1         181902         2         AC13603         AC13603           27         20.2         72.1         181902         2         AC13679         AC136286         AC136079           28         20.2         72.1         181902         2         AC136286         AC	18	20.6					AC055852	Homo sap
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21 20.6 73.6 217584 2 AC112299 AC113299 22 20.6 73.6 218580 2 AC140927 ACC40927 23 20.6 73.6 218580 2 AC140927 ACC40927 24 20.2 72.1 34796 3 CEF53C11 AC136038 26 20.2 72.1 151930 9 CRS1DDVT AC136038 27 20.2 72.1 181934 2 AC132613 AC132913 AC132913 28 20.2 72.1 181974 2 AC136679 AC132913 AC132913 30 20.2 72.1 181970 2 AC138246 AC132948 31 20.2 72.1 224453 2 AC138246 AC134283 32 20.2 72.1 224453 2 AC134283 AC134283 33 20.2 72.1 224453 2 AC13629 BD013428 34 20 71.4 1553 6 BD013422 AB089813 AC126734 35 20 71.4 18556 5 AC126734 AC136134 36 20 71.4 12787 1 AB015654 AC136134 37 20 71.4 188557 9 AC13619 AC126459 38 20 71.4 108582 2 AC126459 AC126459 41 20 71.4 131805 2 AC13648 AC138846 42 20 71.4 131805 2 AC139484 AC139483 44 20 71.4 131805 2 AC139488	C)	20.6				ATFCA8	Z97343 Ar	ą
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23 20.6 73.6 349980 6 AXO44032 AXO44032 25 20.2 72.1 34795 G CEF53CII 25 20.2 72.1 19330 9 CNSOIDVT ALI2931 ALI32913 26 20.2 72.1 116345 2 ACI33913 ACI33913 ACI32913 ACI33913 ACI339130 ACI330130 ACI33	N	20.6	73.6			AC140927	AC140927	Mus muscu
24 20.2 72.1 34796 3 CEF55011 Z79756 CR	23	20.6	73.6			AX044032	AX044032	Sequence
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727 bp DNA linear BCT 07-SEP-1994	gene.	X16045.1 GI:42716 arsenical resietance; arsR gene; ArsR protein; DNA-binding protein;	ance gene.	Escherichia coli Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	ichia.	San Francisco, M.J., Hope, C.L., Owolabi, J.B., Tisa, L.S. and	
RESULT 1 ECRFARSR/c LOCUS SCRFARSR 7	DEFINITION E. coli R-factor R773 arsR gene. ACCESSION X16045	VERSION X16045.1 GI:42716 KEYWORDS arsenical resistance; arsR	regulatory protein; resistance gene. SOURCE Escherichia coli	ORGANISM Escherichia coli Bacteria; Proteobacteria;	Enterobacteriaceae; Escherichia. REFERENCE 1 (bases 1 to 727)	AUTHORS San Francisco, M.J., Hope, C	Rosen, B. P.

ALIGNMENTS

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Furnya, N. and Komano, T.
Determination of the nick site at oriT of Incll plasmid R64: global similarity of oriT structures of Incll and IncP plasmids
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J. Bacteriol. 175 (16), 5035-5042 (1993)
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location of the Nika-binding sequence
J. Bacteriol. 179 (23), 7291-7297 (1997)
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Nucleotide sequence of the rei gene encoding shufflon-specific DNA
recombinase in the Inc11 plasmid R64: homology to the site-specific
recombinases of integrase family
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Submitted (09-AUG-1989) Rosen B.P., Department of Biochemistry,
Wayne State University, School of Medicine, 54- B Canfield Avenue,
Detroit MI 48201, U S.A.
Location/Qualifiers
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Bacteria; Propebbacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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rectrinication of the metalloregulatory element of the plasmid-encoded arsenical resistance operon Nucleic Acids Res. 18 (3), 619-624 (1990)
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Shufflon: multi-inversion of four contiguous DNA
plasmid R64 creates seven different open reading
Nucleic Acids Res. 15 (3), 1165-1172 (1987)
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/note="99 pct identical to sp:ARD1_ECOL1,sp:P46003[ArsD of plasmid R773]" /codon start=1 /trans1_table=11
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RPNLAQQPMSFVQNBKVKAFIEASGAEGLPLLLLDGETVWAGRYPKRAELARWFGIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX321886 169613 bp DNA linear HTG 30-JUN-2003 Danio rerio clone DKEYP-46C9, WORKING DRAFT SEQUENCE, 5 unordered
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Submitted (26-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Submittedshire, (2810 1SA, UK. B-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 1, 2003 this sequence version replaced gi:29603281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(4148, .7818,18208, .20046)
/note="different from Tn5393[gb:M96392] in IS1133 insert
position and terminal direct repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jame = 99 pt identical to pir:A25937[ArsA of plasmid 7773, arsenical pump-driving ATPase]
location 3593. .1597 and location 20833. .20837 are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(3598. .4147,20047. .20832)
/insertion.seq="152"
complement Tjoin(3609. .4147,20047. .20418))
/gene="yadA"
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HTG; HTGS BHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                   join(3542. .3597,20833. .22533)
/gene="arsA"
join(3542. .3597,20833. .22533)
/gene="arsA"
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/gene="arsD"
3162. .3524
/gene="arsD"
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Best Local Similarity
Matches 27; Conserv
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LGYDMYKLHEQQQKRLRESETRQOLI REGYLREDEDI SVHAARKRWYLORSQDALKKR
REKAAASKRANRLKKLPVDQQI YEMAEYLRKRLPPDBAYFCSDDHLKRLAIRELRQLE
                                                                                                                                                                                                                                   Sampei, G., Komano, T., Sasaki, T., Tachibana, K., Puruya, N., Saito, Y., Suzuki, T. and Mizobuchi, K.
Organization and diversification of plasmid genomes: complete
                                                                                                                                                                                                                                                                                                                                                              Komano,T., Sasaki,T., Tachibana,K., Furuya,N., Saito,Y., Suzuki,T.,
Sampei,G. and Mizobuchi,K.
Direct Submission
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HPFYVQKRTFVGRKYAFRPEKQRLLDAIWPVLVSFSDAGTHTVGMSVTRLABEISPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MAGLKNTPYNAVHWSQLAPEEQIRFWEDYEAGRATTFLVEPERK"
                                          Komano, T., Yoshida, T., Narahara, K. and Furuya, N.
The transfer region of Incl1 plasmid R64: similarities between R64
Tra and legionella icm/dot genes
Mol. Microbiol. 35 (6), 1348-1359 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-MAY-2002) Gen-ichi Sampei, The University of Blectro-Communications, Applied Physics and Chemistry; Chofugaoka 1-5-1, Chofu, Tokyo 182-8585, Japan (B-mail: sampei@pc.uec.ac.jp, Tel:81-424-43-5481, Pax:81-424-43-5501)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note==R64 strain drd-11"

/note==R64 strain drd-11"

/note==100 pct identical to sp:YI22_ECOLI[hypothetical protein of insertion sequence 182]

location complement(4143. 4147) and location complement(4143. 4147) and location 378. 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Salmonella typhimurium"
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                                                                                                                                                                                                                                                                                                   nucleotide sequence of R64 genome Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAB91568,1"
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'transl_table=
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378. .467
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455. .1486
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'gene="repY"
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'gene="repz"
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/gene="arsR"
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/gene="arsR"
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Homo sapiens chromosome 17, clone RP11-515017, complete sequence.
AC007638
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Consensus quality: 167966 bases at least Q40 Consensus quality: 168429 bases at least Q30 Consensus quality: 168484 bases at least Q30 Insert size: 169213; sum-of-contigs Insert size: 178871; 3.5% error; agarose-fp Quality coverage: 8.6% in Q20 bases; sum-of-contigs Quality coverage: 8.6% in Q20 bases; sum-of-contigs Quality coverage: 8.6% in Q20 bases; sum-of-contigs Quality Coverage: 9.6% in Q20 bases; sum-of-contigs Q20 bases; 
                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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77.1%; Score 21.6; DB 2; Length 169613;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4166: contig of 4166 bp in length
4266: gap of 100 bp
27503: contig of 23237 bp in length
2503: gap of 100 bp
85675: contig of $8072 bp in length
85775: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 88619: Contig of 2844 bp in length 88719: gap of 100 bp 0 169613: contig of 80894 bp in length. Location/Qualifiers
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-515017 Unpublished
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88720. .169613
/note="assembly_fragment:00756.0"
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1. .4166
1. .4166
1. .4166
fragment chain:1"
4.267. .27503
fragment chain:1"
/note="assembly_fragment:01353
fragment chain:1"
7.00te="assembly_fragment:01353
fragment chain:1"
7.00te="assembly_fragment:01439
fragment_chain:1"
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/db_xref="taxon:7955"
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REFERENCE
AUTHORS
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Direct Submission

Direct Submission

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Direct Submission

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Es 1 [bases 1 to 1820E]

Birren B., Linton, L., Nusbaum, C., Lender, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreitz, P., FiltZhugh, W., Gage, D., Galagan, J., Gardyns, S., Gord, S., Goyette, M., Grana, L., Gardyns, S., Gardyns, S., Gord, S., Goyette, M., Grana, L., Gardyns, S., Landers, P., Filtzaras, A., Karls, C., LaRocque, K., Lamazares, R., Landers, T., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., MacCarn, C., MacGonald, P., Major, J., Marquis, N., Mathews, C., McCarn, C., Noren, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Naylor, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Stenaus, N., Subramanian, A., Yanden, S., Severt, M., Tavis, N., Taslamas, J., Tasfaye, S., Theodore, J., Viel, R., Vo,A., Wilson, M., Travis, N., Taslamas, J., Ye, W.J., Young, G., Zahoun, J., Zembek, L., Zimmer, A. Taslamas, J., Ye, W.J., Young, G., Shibhi, L., Zimmer, A. Taslamas, J., Ye, W.J., Young, G., Shibhi, L., Zimmer, A. Taslamas, Therefore, J., Young, G., Shibhi, L., Zimmer, A. Taslamas, J., Tasfaye, S., Theodore, J., Viel, R., Wolf, W., Willen, A., Wann, C., Wann, L., Zahoun, J., Wann, Wallen, M., Wann, M., Ye, Wann, C., Young, G., Shibhi, L., Zimmer, A., Taslamas, J., Ye, W.J., Young, G., Simbek, L., Zimmer, A. Taslamas, J., Tasfaye, J., Young, G., Shibhi, L., Zimmer, A. Taslamas, J., Tasfaye, J., Young, G., Shibhi, L., Zahoun, J., Wann, M., W
Submitted (02-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 2, 2001 this sequence version replaced gi:13958524. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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------ Project Information
Center project name: £458
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Web site: http://www-seg.wi.mit.edu
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Center clone name: 515_0_17
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/rpt_family="MIR"
21287. 21593
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complement (21594. 21750)
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ACU9U562

73000 bp DNA linear HTG 03-MAR-2001
HOMO Sapiens Chromosome 5 clone RP11-403N11 map 5, LOW-PASS
SEQUENCE SAMPLING.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barnen, B., Linton, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [ [bases 1 to 73000] Birran,B. Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 5, clone RP11-403N11
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  Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehozky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marthews, C., MacLethy, M., McDwan, P., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Minova, T., Menga, V., McDheeters, R., Meldrim, J., Meneus, L., Minova, T., Menga, V., Murphy, T., Naylor, J., McMil, D., Oliver, J., Peterson, C., Oromor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, R., Phukhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Stougez, C., Spencer, B., Schauer, S., Schuback, R., Stanger, S., Schauer, S., Trayser, M., Trayis, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Traves, M., Travis, N., Trayis, N., Tra
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* sequencing reads that have not been assembled into
* contiggs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
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Homo sapiens BAC clone RP11-462D9 from 8, complete seguence.
ACO20553
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Submitted (03-JAN-2000) Genome Seguencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 160811)
Waterston, R.H.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160811)
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Submitted (17-JUN-2000) Genome Sequencing Center, Washington
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Harkins,R., Hawkins,M., Drone,X. and Myers,M.
The sequence of Homo sapiens BAC clone RP11-462D9
Unpublished
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Toward a complete human genome sequence
Genome Res. B (11), 1097-1108 (1998)
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Pred. No. 1.8e+
0; Mismatches
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Waterston, R.H.
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SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-462D9;
Location/Qualifiers
irce
1.160811
University School of Medicine, 4444 Forest Park Parkway, St. Louis, MG 52108, USA
S. (bases 1 to 160811)
Waterston, R.
Direct Submission
Submitted (O7-007-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jun 17, 2000 this sequence version replaced gi:7631006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30; an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTICE: This sequence may not represent the entire insert of this close. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between naighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPPING INPORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. L.
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                      ------ Genome Center
Center: Washington University Genome Sequencing Center
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Contact: sapiens@watson.wustl.edu
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/mol type="genomic DNA"
/db_xref="taxon:9606"
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/rpt_family="L1"
2004. 3092
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/rpt_family="MaLR"
44775 .4775
/rpt_family="Alu"
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6523. .8335
/rpt_family="L1"
10561. .10951
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31645 .31855
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32674 .32865
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1006. .31398
                                                  11669...12155

(Tpt family="BRVL"

1204 ...12376

/Tpt family="ERVL"

12402...13063

/Tpt family="ERVL"

13205...13609
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17875. 18247

17073. 19324

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13340. 19542

1764 family="Alu"
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22868. 23001
/ rpt family="12"
23765. 24143
/ rpt family="MALK"
24144. 24769
/ rpt family="RVI"
25553. 2556
/ rpt family="12"
2556. 2756
/ rpt family="11"
2756. 2773
/ rpt family="11"
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/ rpt family="11"
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15053..15155
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33813, .34024
/rpt_family="BRV1"
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The sequence of Mus musculus clone
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Upact Submitted (20-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Direct Submitted (20-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Wilson, R.K.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Contact: submissions@watson.wustl.edu
Contact: submissions@watson.wustl.edu
Center project name: M_BB0276M02
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                     rpt family="L1"
5254. .36027
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                                                                                                             TITLE
JOURNAL
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AUTHORS
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Statusty, D. Marie, Metzer, M. Lee., Abramizon, S., Addams, C., Alder, J., Alber, Metzer, M. Lee., Abramian, D., Angulano, D., Cardens, C., Carder, M., Chen, G., Coyle, M., Cese, J., Denora, D., Davila, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M., Davis, C., Davis, C., Davis, C., Davy-Carroll, L., De Anda, C., Dever, M., Carada, M., Davis, C., Penlayano, D., Gerre, G., Bandleo, D., Davis, C., Penlayano, C., Serie, M., Hanla, C., Hanliton, K., Davis, D., Harnandez, S., Hadun, S., L., Hadgon, M., Hernandez, M., Hanla, C., Hanliton, C., Hamilton, K., Harnandez, M., Hanland, M., Hally, S., Haldun, S. L., Haddun, S. L., Haddun, S. L., Hogson, A., Hogues, M., Hernandez, R., Hinles, S., Hillyk, S., Kally, S., Kally, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kally, S., Kally, S., Kally, S., Kelly, S., Kelly, S., Kelly, S., Kally, S., Munded, M., Malloud, M., Malloud
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC118161 177109 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-296C3, WORKING DRAFT SEQUENCE.
AC118161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                       75.7%; Score 21.2; DB 10; Length 174303; 88.5%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                              Indels
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                            64759 ACACATAACCAAGCAGCATATGATT 64784
/mol_type="genomic DNA"
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/chromosome="18"
/clone="RP24-276M2"
                                                                                                                                                                                                                                                                                        3 ACACATAACCAAAAACGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 177109)
                                                                                                                                                                                                                              23; Conservative
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                                                                                                                                                                                                  Similarity
                                                                                                                                                                       Query Match
                                                                                                                                                                                                        Best Local
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AC118161
LOCUS
DEFINITION
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KEYWORDS
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Direct Submission

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:22856412.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table bollow represents a scaffold in the Atlas assembly (a 'contig solow represents a scaffold in the Atlas individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                      Submitted (14-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap; version 0.990329
Consensus quality: 172459 bases at least Q40
Consensus quality: 17361 bases at least Q30
Consensus quality: 17750 bases at least Q30
Estimated insert size: 177946; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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------- Project Information
Center project name: QAU
Center clone name: CH230-296C3
Center clone name: CH230-296C3
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/note="wgs_contig"
                                                                                                                                                                                                                                (bases 1 to 177109)
                                                                                                                                                       Direct Submission
Unpublished
                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
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Matches 23; Conserv
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Research
                                               Center: Whitehead Institute/ MIT Center for Genome
  Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                Center code: WIER
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 110585
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note="<30 qual single clone coverage"
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/note="<30 qual single clone coverage"
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/note="<30 qual SNGL region"
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/note="<30 qual SNGL region"
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/note="<30 qual SNGL region"
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P. (1996-1997)
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complement (6291. 6990)
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complement (7131. 7472)
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7615. 7654
                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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067, .5300
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complement (4052. .4253)
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complement (4601. .4992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147. .194
/rpt_family="AT_rich"
                                                                                                                                                                                                             Center clone name: 42_C_24
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/note="<30 qual SNGL
                                                                                                                                                                                                                                                     Location/Qualifiers
1. .184897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="LTR33"
854. 3103
                                                                                                                                                                                                                                                                                                                                                                              'chromosome="8"
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                                                                                                                                               ACD90919 184897 bp DNA linear PRI 24-JAN-2002
Homo sapiens chromosome 8, clone RP11-42C24, complete sequence.
AC090919
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184897)
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                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-42C24 Unpublished
                         79933 ACACATATCCAAACAGGCATATGATT 79958
  3 ACACATAACCAAAAACGCATATGATT 28
                                                                                                                                                                                                                                 AC090919.6 GI:18308311
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                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                             DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                          ORGANISM
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AUTHORS
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The There's Allen, H., Alsbrooks, S., Amin, A., Angurano, D., Anyalebechi, V., Anyali, A., Angurano, D., Anyalebechi, V., Anyali, A., Angurano, D., Anyalebechi, V., Anyali, A., Angurano, D., Bandarani, A., Angurano, D., Bandarani, A., Babbachi, B., Barber, M., Barnstead, M., Benahmed, F., Biswalo, S., Bandarani, A., Blankehburn, K., Blyth, P., Brown, M., Blyth, P., Brown, M., Calderon, B., Cardens, V., Carter, K., Cavazo, I., Casar, H., Canter, A., Chan, J., Cardens, W., Carter, K., Cavazo, I., Casar, H., Canter, A., Durano, C., Dang, Y., Carter, M., Canter, M., Canter, M., Carter, M., Durano, C., Dang, Y., Dinh, H., Diva, A., Davilla, M., Davilla, M., Darano, C., Ding, Y., Dinh, H., Diva, A., Marano, M., Darish, M., Cable, M., Banillo, M., Durbis, L., Poster, M., Gabris, R., Garte, M., Hondrandez, J., Handes, S., Hadun, S., Hadun, S., Hadun, S., Hande, J., Idhan, M., Jang, M., Jang, M., Jang, H., Wases, A., Henderson, M., Barnandez, J., Liu, W., Martin, R., Marti
Rattus norvegicus clone CH230-42L16, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces. AC130151
AC130151. 4 GI:30522322
HTG; HTGS PHARFI: """."
                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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2 (bases 1 to 199985)
Worley, K.C.
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complement (2366. ..23870)
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complement (2381. ..23870)
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complement (2451. ..2576)
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complement (2561. ..2662)
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complement (2663. ..26690)
/rpt family="LiM4c"
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23776. .23789
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CompTemily="Tigger2"
compTement(17232..17871)
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compTement(17878..18175)
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complement (15527. .15641)
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15642. .15725
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complement (9747. .9805)
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13026. 13785
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complement(7827, .8)
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TITLE Direct Submission
JOHNAL Unpublished
REPERENCE 2 (bases to 199985)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 199985)
AUTHORS RA Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department

109325 ACACATAACAAAAAAGCTTATGATT 109350

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RESULT 10 AC130151/c PAT 07-JAN-2002

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Neisseria meningitidis MCSB

Neisseria meningitidis MCSB

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Neison, K.J., R., Bisen, J.A., Ketchum, K.A., Hood, D. W., Peden, J. F., Pelson, K.J., Neison, K.J., Mitch, O., W., Peden, J. F., Codson, R.J., Neison, R.J., Mitch, O., Fleischmann, R.D., Dougherty, B.A., Mason, T. (Glecko, A., Parksey, D. S., Blair, B., Cittone, H., Clark, B.B., Cotton, M.D., Utterback, T.R., Khouri, H., Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappoli, R. and Vener, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis serogroup B strain MC58 section 131 of 206 of the complete genome.
AE002489 AE002098
AE002489.1 GI:7226640
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Direct Submission
Submitted (17-MAR-2000) The Institute for Genomic Research, 9712
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Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           1. .6391
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                                                                                                                                                                                                                                                                               Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with dna transcription Parent: WO 0192565-A 11 06-DEC-2001; Epigenomics AG (DE)
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Sequence 11 from Patent W00192565.
AX323523
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On May 10, 2003 this sequence version replaced gi:25009137.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.fmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and the feature table.
                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 6 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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88.5%; Pred. No. 1.5e+02;
iive 0; Mismatches 3;
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                                                           COMMENT
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                                                                                                                                                                                                                                                                                                                                  SSS
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     source
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MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the MHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu
                                                                                                                                                                                                                                     not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, F. Tateno, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries, Genomics 511-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The clone sequenced to the left is CTB-22X14, 2000 bp overlap the clone sequenced to the right is CTD-2009F14, 2000 bp overlap. Actual start of this clone is at base position 54039 of CTB-22X14 actual end is at base position 9162 of CTD-2009F14.
  NEIGHBORING SEQUENCE INFORMATION:
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5389. .5659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restriction digest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (18-SEP-2001) Genome Sequencing Center, Washington
Nuversity School of Medicine, 4444 Porest Park Parkway, St. Louis,
MO 63108, USA
(bases 1 to 65542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Submitted (08-OCT-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 65542)

Sulston, J. E. and Wilson, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Homo sapiens BAC clone RP11-393L14 from 7, complete sequence.
AC091766
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                                                                                                                                                                                                                                                                                                                                                                          Length 10099;
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Abboct,A. and Shah,N.
The sequence of Homo sapiens BAC clone RP11-393L14
Upublished (2001)
3 (bases 1 to 65542)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                    Indele
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6 (bases 1 to 65542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Genetics,
                                                                                                                                                                                                                                                                                                                                                                   Score 20.6; DB 1;
Pred. No. 4.4e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                          product="IS1016C2 transposase"
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Submitted (29-APR-2003)
University, 4444 Forest
7 (bases 1 to 65542)
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                                                                                                                                                                                                                                                                                                                                                                     73.6%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.27
Conservative
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone ame. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was fanished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: FMBL; Sw: SWISSPROT; Tr: TREMEL; Mp:, WORMPEP; Information on the WORMPEP databases can be found at the their source databases:

from the RPCI-23 Mouse BAC Library and an annother and the sequence of the sequence of the sequence that the feature the sequence of the sequence of the feature table with their source databases:

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Mouse DNA sequence from clone RP23-75B19 on chromosome 2, complete
sequence.
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
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For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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E (Dases 1 to 121636)

Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Kim, D. and Roe, B.A.

Direct Submission

Numbrited (123-MAY-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
Ok 73019, USA

S haull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Kim, D. and Roe, B.A.

Direct Submission

Submitted (18-DBC-2003) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

On Dec 18, 2003 this sequence version replaced gi:39930621.
                                                                                                                                                                                                                                                                                                                                                                                                             AC122166 121636 bp DNA linear HTG 18-DEC-2003
Medicago truncatula clone mth2-33b23, WORKING DRAFT SEQUENCE, 5
unordered pieces.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Pabales, Pabaceae, Papilionoideae, Trifolieae,
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1 (Dases 1 to 121636)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-33b23
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                                                                                                                                                                  Query Match 73.6%; Score 20.6; DB 10; Length 110685; Best Local Similarity 85.2%; Pred. No. 2.8e+02; Matches 23; Conservative 0; Mismatches 4; Indels 0;
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5310 5309: app of unknown length
5709 15808: gap of unknown length
5709 24261: contig of 10399 bp in length
5809 24261: contig of 8453 bp in length
4352 44670: contig of 8653 bp in length
4571 44770: app of unknown length
4771 app of unknown length
6771 121636: contig of 76866 bp in length.
Location/Qualifiers
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The University Of Oklahoma
Center code: UOKNOR
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Medicago truncatula (barrel medic)
Medicago truncatula
/mol_type="genomic DNA"
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May 26, 2004, 15:20:44 ; Search time 584.231 Seconds (without alignments) 3115.905 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                   3470272 seqs, 21671516995 residues
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Listing first 45 summaries
                                                            OM nucleic - nucleic search, using sw model
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1 Diorio,C., Cai,J., Marmor,J., Shinder,R. and DuBow,M.S. An Escherichia coli chromosomal ars operon homolog is functional in

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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arsenic detoxification and is conserved in gram-negative bacteria
J. Bacteriol. 177 (8), 2050-2056 (1995)
95238276
                                                                                                                                 2 (bases 1 to 3492)
Diorio, C.
Direct Submission
Submitted (06-JUL-1994) C. Diorio, McGill University, 3775
University Street, Montreal, Quebec, H3A 2B4, CANADA
Location, Qualifiers
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655. . 1061

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AUTHORS
TITLE
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1 (bases 1 to 10240)
Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Mau, B. and Shao, Y.
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This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG01301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently denomed fermined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneWark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Allanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blattner, F.R.
Direct Submission
Direct Submission
University of Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
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Variable (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.

Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB000426 10240 bp DNA linear BCT 01-DBC
Escherichia coli K12 MG1655 section 316 of 400 of the complete
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100.0%; Pred. No. 0.00044;
ive 0; Mismatches 0; Indels C
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2910. .2923
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Plunkett, G. III.
Direct Submission
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Blattner, F.R.
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Escherichia coli X12
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Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by conrelating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli KI2 sequence and its annotations are periodically updated; this is version M94. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of albebs. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGSVVMI FVCAMLANDEVANLVI IVLSIVVTI IFRQARKIDKTERNKMFVAFVLAV
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COCD19mnt (1679. 2431)
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SLAPVTADRFGYSVYTNLCGAGLIIALLVYIACRGMYKDIGSRPDFRPMSFSKLLYVL
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equal length to YHIP_ECOLI SW: P36837"
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/transl_table=11
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YHIO ECOLI SW: P37633 but has 32 additional N-ter
residues; gtg start, alternate starts possible"
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ILQIELAVLPDSDRRGMTASGHIVINPPWKLEQQMMNVLPWLHSKLVPAGTGHATVSW
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                                    /note="f680; 100 pct identical to OPDA_ECOLI SW: P27298; CG Site No. 18031" /codon start=1
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complement(2754...3029)
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DYSNI PTVVP SHPPI GTVVGI FEGI YAGOTARQA OGDOVKVYKSSFTAMYTAVTTHRQPCRMK
LVCVGPEEKI VGI HGI GFGMDSMLQGFAVALTAVGATKKOFDNTVAL HPPAAEBFVTMR
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Direct Submission Q. Man, Y.M. and Hou, Y.D.

Submitted (08-MAY-2001) Microbial Genome Center of Chinese Ministry of Public Health, 100 YingXin Jie, XuanMu Qu, Beijing 100052, P.R. China
Shigella flexneri 2a str. 301
Shigella flexneri 2a str. 301
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella
1 (bases I to 11524)
Jin, Q., Yuan, Z.H., Xu, J.G., Wang, Y., Shen, Y., Lu, W.C., Wang, J.H.,
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Colang, B.Q., Wen, Y.M., Hou, Y.D. and Yu, J.
Chen, S.S., Wa, D.L.,
Chen, S.S., Wa, D.L.,
Chen, S.S., Ma, D.L.,
Conne sequence of Shigalla flexneri 2a: insights into
Dathogenicity through comparison with genomes of Escherichia coli
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                                                                                                                                                                                                                                                                                                      Length 10240;
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/organism="Shigella flexneri 2a str. 301"
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Nucleic Acids Res. 30 (20), 4432-4441 (2002)
                                                                                                                                                                                                                                                                                                           Score 42; DB 1; I
Pred. No. 0.00038;
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57. ,1419
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AE015361.1 GI:24053992
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Conservative 0;
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Best Local S:
Matches 42
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VERSION
KEYWORDS
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AUTHORS
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TITLE

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AC145934

ITTON Gallus gallus chromosome UNK clone CH261-4211, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.

ITON AC145934.1 GI:33386884

N AC145934.1 GI:33386884

DS Gallus gallus (chicken)

ITSM Gallus gallus

ITSM Gallus gallus.

ITSM SACTOR (Chicken)

ITSM Gallus (chicken)
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Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
                                                 Gaps
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  Length 11524;
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1256: gap of unknown length
2558: contig of 1282 bp in length
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3948: contig of 1190 bp in length
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6401: contig of 1035 bp in length
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6501: gap of unknown length
7599: contig of 1098 bp in length
7599: gap of unknown length
7591: gap of unknown length
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Web site:http://genome.wustl.edu
Contact: submissions@waston.wustl.edu
Center project Information
Center project name: J_AM042101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of Gallus gallus clone Unpublished
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Wilson, R. K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was determined as part of the B. coli Genome Project (Prederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award #G00301 from the NIH Human Genome Project. The entire sequence was independently determined from B. coli MG1655, overlaps and conflicts with other sequence determinations are annotated. The start of this entry overlaps the start of the entry ECUMR2 (L10328) by 547 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bacherichia coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
I (Dases I to 225419)
Sofia, H.J., Burland, V., Daniels, D.L., Plunkett, G. III and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-MAR-1994) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Analysis of the Escherichia coli genome. V. DNA sequence of region from 76.0 to 81.5 minutes
Nucleic Acids Res. 22 [13], 2576-2586 (1994)
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complement(<1. .1085)
                                                                                                                                                                        ECCUW76 25419 bp DNA linear B
E. coli chromosomal region from 76.0 to 81.5 minutes.
U00039
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Plunkett,G. III.
Direct Submission
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ECOUW76
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SOURCE
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VDSEK**
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 242495)
                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (01-M040-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
J (bases 1 to 242495)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (04-MOV-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
On Nov 4, 2003 this sequence version replaced gi:33387136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 6 concigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as true of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1269: contig of 1269 bp in length
1369: gap of unknown length
2935: contig of 1566 bp in length
3035: gap of unknown length
4616: contig of 1581 bp in length
4716: gap of unknown length
6231: contig of 1575 bp in length
6331: gap of unknown length
8354: contig of 1863 bp in length
8354: contig of 234141 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13, 08
Sequencing vector: plasmid; 1008
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least Q40
Consensus quality: bases at least Q20
Consensus quality: bases at least Q20
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                                                                                                                                                                                                                            The sequence of Pan troglodytes clone Unpublished
2 (bases 1 to 242495)
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PROGRESS ***, 6 unordered pieces.
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                                                                HTG; HTGS PHASB1.
Pan troglödytes (chimpanzee)
Pan troglodytes
                                          AC146183.2 GI:38154191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="mRNA start determined by S1 mapping; Molecular Microbiol. 2:767 (1988)"
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/note="includes pho box"
/note="includes pho box"
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6845. .6846. .05516; CC in X13141 and here"
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trans[_table=
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Best Local Similarity 100.0%;
Matches 42; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="ugpB"
                                                                                                                                                                                                                                                                                                                                                                                                     gene="ugpB'
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AC146183
LOCUS
DEFINITION
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B3554"

(codon start=1

/transl_table=11

/product="hypothetical protein"

/protein id="AAR19149.1"

/protein id="AAR19149.1"

/db xref="GI:3004349"

/translation="MILPGRLRRKGILQACPGLSISRQTRVCRCALFLGERSKKMATG

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/translation="MILPGRLRRKGILQACPGLSISRQTRVCRCALFLYGERSKKMATG

/processin id="Milpgrlrghtgl"

/processin i
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/product="putative dehydrogenase"
/product="putative dehydrogenase"
/product="putative dehydrogenase"
/prodein id="ARD19150.1"
/db_xref="G1:30043430"
/db_xref="G1:300430"
/db_xref="G1:3004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="yiaD"
/locus_tag="S4183"
/function="putative membrane, Not classified"
/note="residues 1 to 208 of 208 are 88.94 pct identical to
residues 12 to 219 of 219 from Bscherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /producT="putative outer membrane protein"
|protein_id="AAR19131.1"
|/db.xref="GI:30043431"
|/translation="MSGALAVSGCTTNPYTGEREAGKSAIGAGIGSLVGAGIGALSSS
YORKGKGALIGAAGAALGGGCYGYYMDVQEAKLINDRWGTGVSVTRESCDNIILNMPNN
VTEDSSSAPLKPAGAALGGCCYGYYMDVIKEYPRTANNYIGYTDSTGGEDLAMRESQQRADS
VASALITQGVDASRIRTGQGLGPANPIASNSTABGKAQNRRVEITLSPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ξ
/product="hypothetical protein"
/protein.id="AAP19148.1"
/db_xref="G1:3004348.1"
/translation="MEYXDPMHBLLSSLRQIVFKDBTQKITLTHRTTSCTBIEQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus tag="S4182"
/function="putative enzyme; Not classified"
/note="residues 1 to 324 of 324 are 94.13 pct identical residues 5 to 328 of 328 from Escherichia coli K-12: B353"
                                                                                                                                                                                                                                                                                                                                                                                                             276 of 276 are 94.56 pct identical
276 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759 of 759 are 98.78 pct identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus rag="84184"
/function="enzyme; Biosynthesis of cofactors, carriers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="yiaE"
/locus_tag="S4182"
complement(2215. .3189)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="84183"
complement(3293. .3919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (2215. .3189)
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                                                                                                                                                                                                                                                                                                                                                             /locus tag="S4181"
/note="residues 1 to
residues 1 to 276 of
                                                                                                                                                                 1335. .2165
/gene="yiaP"
/locus_tag="S4181"
1335. .2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus tag="S4184"
4160. .6439
/gene="bisC"
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/transl_table=:
                                                                                                                                                                                                                                                                                                                                  'gene="yiaF"
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/gene="bisC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="yiaB"
                                                                                                                                                                     gene
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Shigella flexneri 2a str. 2457T
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
Enterobacteriaceae; Shigella.
Enterobacteriaceae; Shigella.
Enterobacteriaceae; Shigella.
Enterobacteriaceae; Shigella.
Shigella.
Fournier,G., Mayhew,G.P., Plunkett,G. III, Rose,D.J., Darling,A., Rau,J. Perna,N.T., Payne,S.M., Runyen-Janecky,L.J., Zhou,S., Schwartz,D.C. and Blattner,F.R.
Complete Genome Sequence and Comparative Genomics of Shigella flexneri Serotype 2a Strain 2457F
Infect. Immun. 71 (5), 2775-2786 (2003)
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of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MSGKMTGIVKWFNADKGFGFITPDDGSKDVFVHFSAIQNDGYKS
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/note="residues 1 to 41 of 41 are 100.00 pct identical to
residues 1 to 41 of 96 from Escherichia coli K-12 : B3555"
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Wei,J., Goldberg,M.B., Burland,V., Venkatesan,M.M., Deng,W.,
Pournier,G., Mayhew,G.F., Plunkett,G. III, Rose,D.J., Darling,A.,
Mau,B., Perna,N.T., Payne,B.M., Runyen-Janecky,L.J., Zhou,S.,
Schwartz,D.C. and Blattner,F.R.
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/transī table=11
/product="cold shock protein 7.4, transcriptional
activator of hns"
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Submitted (13-JUN-2002) Genetics Laboratory, University (Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, 1 Location/Qualifiers
1. .289816 /organism="Shigella flexneri 2a str. 2457T"
                                                                                                                          ö
                                  ch 100.0%; Score 42; DB 2; Length 242495; Similarity 100.0%; Pred. No. 0.00026; 42; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
of 16 o
                                                                                                                                                                                                                                                        3312 CTGCACTTACACATTCGTTAAGTCATATATGTTTTGACTTA 3353
                                                                                                                                                                                                        1 CTGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
section 15
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complement (896. .1021)
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complement (238 . 450)
/gene="cspA"
/locus tag="84179"
complement (238 . 450)
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db xref="GI:30043427"
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/strain="24577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE016992 289816 bp
Shigella flexneri 2a str. 2457T
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complement (896. .1021)
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/transl_table=11
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AE016992 AE014073
                                                                          Best Local Similarity
Matches 42; Conserv
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                                           Query Match
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AE016992/c
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JOURNAL
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KEYWORDS
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/gene="gor"
/function="enzyme; Biosynthesia of cofactors, carriers:
/function="negoxin, glutaredoxin, glutathione"
/note="Residues 1 to 450 of 450 are 99.33 pct identical to
residues 1 to 450 of 450 from Escherichia coli K-12 Strain
MG1655: B3500"
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/transl_table=11
/product=glutathione oxidoreductase*
/product=glutathione oxidoreductase*
/brotein_id="AAG58632.1"
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/GCVPKKVWWHAAQIREAHHYGPDQFDTIINKFWMFTLIASRTAYIDRIHTSYENV
/GKNNVDVIKGFARFYDAXTLEANGSTITADHILIANGGRESHPDIFGVEYGIDSDGF
FALPALPERVAVVGAGYIAVELAGVINGLGAKTHLEVRKHAPLRSFDPMISETLIVEVM
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WYRTBKGY TVUDKYQNTNYBGI YAVGDNTGAVELTPVAVAGRRLSERL FNNKPBEHL
DYSNI PTVVPSKHP I GTVGLTEPQRRQYGDDQVKYKSSFTAWY TAYTHRQPCRWK
XVCVGPEBKI VGIHGIGFGMDEXLQGFAVALLEMENTYAIHPTAAEEFVTNR
                                                                                                                                                                                                                                               DNA linear BCT 21-MAR-2001
genome, contig 3 of 3, section 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaroteobacteria; Enterobacteriales; Enterobacteria; Daniela; Enterobacteria; Daniela; Enterobacteria; Daniela; Enterobacteria; Daniela; 
                                    66064 CIGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 66023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2300. .2653
/gene="arsR"
/note="arsn"
2300. .2653
/gene="arsR"
                                                                                                                                                                                                                                               AE005575
Escherichia coli 0157:H7 EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bscherichia coli 0157:H7 EDL933
Escherichia coli 0157:H7 EDL933
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/note="synonym: Z4900"
                                                                                                                                                                                                                                                                                                                                                                 AE005575 AE005174
AE005575.1 GI:12518196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67. .1419
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                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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MEDLINE
PUBMED
REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
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SOURCE
                                                                                                                                                              RESULT 8
AE005575
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                                    임
                                                                                                                                                                                                                                                                                                      /jocus tag="S4186"
/function="enzyme; DNA - replication, repair,
/function/modification:
/note="residues 1 to 187 of 187 are 97.32 pct identical to
residues 1 to 187 of 187 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus rag="S4185"
/note="residues 1 to 146 of 146 are 97.94 pct identical to
residues 1 to 146 of 146 from Escherichia coli K-12 :
B3550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MIRBAQRSELPAILEELMLESTFWGHPFIKANYWRDCIPLVRDAY
LANAQWWWEBEGKLLGFVSINGGRFLAAMFVAPKAVRRGIGKALMQYVQQRYPHLML
EVYQKNQPAIDFYRAGFHIVUCAWQDETQLPFWIMSWPVVQTL"
complement (6845...7408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tränslation="MERCGWVSQGPLYIAYHDNEMGVPETDSKKLFEMICFEGQAGGL
SMYTVLKKERNYRAYFHQPDPVKVAAMQEEDVERLVQDAGIIHHRGKLQAIIGNARAY
LQMEQAGEPFPDFYMSFVMHQPQYTQATTLSBIPTSTSASDALSKALKKRGFKFVGTT
ICYSFMQACGLVNDHVVGCCCYLGNKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Jocus frag="S4187"
/function="putative enzyme; Not classified"
/note="residues 1 to 232 of 232 are 99.13 pct identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
to residues 1 to 739 of 739 from Bscherichia coli K-12
B3551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Score 42; DB 1; Length 289816;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 42; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/produce="n=ethyl-adenine DNA glycosylase I"
/protein_id="AAR19154.1"
/db_xref="GI:30043434"
                                                                                                                                                /transI_table=11
/product="botin sulfoxide reductase"
/protein id="App19152.1"
/db_xref="GI:30043432"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trans1_table=11
/product="hypothetical protein"
/protein id="AAP19153.1"
/db_xref="GI:30043433"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="tag"
/locus_tag="S4186"
complement(6845. .7408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="S4185"
complement(6408. .6848)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fgene="yiaC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="yiaC"
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SGS

1 CTGCACTTACACATTCGTTAAGTCATATGTTTTTTGACTTA 42

8

gene

9

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/gunction=orf, Unknown function"
/functe="Residues 1 to 176 of 176 are 99.43 pct identical to casidues 1 to 176 of 176 are 99.43 pct identical to more assidues 1 to 176 of 176 from Escherichia coli K-12 Strain MG165: B3507"
/codon start=1
/transl_table=11
/product="orf, hypothetical protein"
/product="orf, hypothetical protein"
/db_xref="G1:12518204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAG58638.1"
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/translation="MVLIFURDSNMNWTKGALILSLSFLLAACSSIPQNIKGNNQPB
IQKSFVANHUQGLYVGQARFGGKVINVINGKTDTLLEIAVLPLDSYAKPDIEANYQ
GRLLARQSGFLDPPYNYRNHFYTILGTIQGEQPGFINKVPYNFLEVNMQGIQVMFLREV
VNTTYNLMDYGYGAFWPEPGMGAPYYTNAVSQVTPELIVK"
                                                                             /protein_id="aags8637.1"
/db_xref="G1:12518202"
/db_xref="G1:12518202"
/db_xref="G1:12518202"
/db_xref="G1:12518202"
/db_xref="G1:12518202"
/translation="MSIDFFGMINTYHGDIYNRTTDTDNVKTPDTPWPCDNREEQQPINSTBS1SEGSYNPEGYPLAAQH:POTYACRTNTKYTDADYSKVVAQUVSLITNIESISSTPLTRQAQEILAQINNIRYEKNKSAECRIIVVANPKPDKAIITKISVEGIPVRFSV
                                                                                                                                                                                                            OTMFSDTNFIAEQRADLPTNIKDIQSLYQKMTKLYIEHSENKORMKVFAGTNFIDFNM
TOGNIGGEVTUTLSRPYEDDLIAINFPDALGOPIFSHKEHPTPRLYKDSQYLDKQTEG
LESTLLTINDNFLARKAEIASTIIKFLARAITNLSYXDILKYQQEFQKECYKQVKSFT
TLSRYNKIQTWAEMSEYQFEVPQYETINPKKCHARII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to 199 of 199 are 99.49 pct identical to of 199 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MFLIITRDTMFFTAMKNILSKGNVVHIQNEEIDVMLHQNAFVI
INDNILMNNFSNFLYQIERLKEVHVIIFSPFNIKRCLGKVPVTFVPRTITIIDFVALI
NGSYCHPEANVSLSKKQHQVLSCIANQMTTEDILEKLKISLKTFYGHKHNIMMILKL
KRINELVRHQHIDYLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Bscherichia coli O157:H7 DNA, complete genome, section 16/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7786. .>11071
/note="O-island #140; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655"
complement(7845. .8873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon start=1
/transl_table=11
/product="outer membrane protein induced after carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="slp"
/function="membrane; Cell envelop: Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="chus"
/function="putative transport; Transport of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym: Z4910"
complement(7845..8873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: Z4909"
7254. .7784
/gene="yhi?"
                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: Z4908"
6499. .7098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Residues 1
residues 1 to 199
WG1655: B3506"
                                    /protein id-p-
             /transl +---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constituents"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene≈"yhiF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="chuS"
                                                                                                                                                                                                                                                                                                                      6499. .7098
/gene="slp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             starvation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7254. .7784
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Best Local Similarity
Matches 39; Conserv
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AP002565
LOCUS
DEFINITION E
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                                                                                                                                                                                                                        /protein_id="AAGS8633.1"
/db_xref="G1:12518198"
/fb_xref="G1:12518198"
/franslation="MSFLPTQ1FKILADETRLGIVLLISELGELCVCDLCTALDQSQ
/franslatireseGillDrkQGKWVHYRLSPHIPSWAAKLIEQAWRCEQEKVQVIVRN
LARQNCSVDSKNTCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="Milagal FVLTIVIVINOPKGLGIGWSATLGAVLALVTGVVHPG
DIPVWNIVMXATAARTAYIISLLDESGRFEWAALHVSFWGNGRGLLFFWIVLLG
AAVAALFANDGAALILFPIVIAMLLALGESKGFTLAFVWAGRFGIADTASDFILLSSDFILWIVL
NIVSADFFGLGFREXSVWPVDIAALVATLWHLHYFRKDIPONTDWALLKSPARAL
KDPATFKTGWVVLLLLLWGFFVLEPLGIPVSAIAAVGALILFVVAKRGHAINTGKVLR
RANMYTVLVGALSINGSTASGVIKEAMYTANTGCDLGPKTTPIGSLAFLSSI
MNNMFYLVGALSINGSTASGVIKEAMYTANTGCDLGPKITPIGSLAFLSSI
KNMTISWGYYFRIGIIMTLPVLFVTLAALALRLSFTL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sensitivity"
/note="Residues 1 to 141 of 141 are 98.58 pct identical to
residues 1 to 141 of 141 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/KLIADMGISYRALIERRYNEPYEELGIAEDRYTDDEILDFMLQHPILINRPIVYTTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5062. .6177
/function=10xf; Unknown function"
/note="Residues 1 to 249 of 371 are 89.95 pct identical to
residues 1 to 249 of 260 from Escherichia coli K-12 Strain
                                                       /note="Residues 1 to 117 of 117 are 94.87 pct identical to residues 1 to 117 of 117 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Residues 1 to 429 of 429 are 100.00 pct identical to residues 8 to 436 of 436 from Escherichia coli K-12 Strain MG1655: B3502"
function="regulator; Protection responses: Drug/analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="transport; Protection responses: Drug/analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4009. .4434
/gene="arsC"
/note="synonym: 24905"
4009. .4434
/gene="arsC"
/function="enzyme; Protection responses: Drug/analog
                                                                                                                                                                              /product="transcriptional repressor of chromosomal operon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAGS8636.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Z4906"
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gene

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ANSETPI SDALTWI PALGSTAGI FVA JITAMI VILGSLSSCWYYGPRELESAMAKKNEF
KCPGEVYPRXYNT PDVSI ILGGALGI PPI PVSDLTSLLGYFTL WHCFKYTLTFGSI IW
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YTVAAGPLRPLGYRTAPHAEIGKI KNDLKQLPNALGYLVTATBEKGRUGDELASMPHI
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C-terminal part (162-294 in 294 aa) is similar to
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3045. .3872
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Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Makino,K., Okoyama,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Sanakawa,C. and Shinagawa,H.
Sanakawa,C. and Shinagawa,H.
Complete nucleotide sequence of the prophage VT2-Sakai carrying the
verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
derived from the Sakai outbreak
Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                               Escherichia coli 0157:H7
Bacherichia coli 0157:H7
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacees; Escherichia.
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Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comparative analysis of the whole set of rRNA operons between an enterchemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655 Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
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Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
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                                   GI:13363693
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  AP002565 BA000007
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Welch, R.A., Burland, V., Plunkett, G.D. III, Redford, P., Roesch, P., Rasko, D.A., Burland, V., Plunkett, G.D. III, Redford, P., Roesch, P., Rasko, D.A., Buckles, E.L., Liou, S.-R., Boutin, A., Hackett, J., Stroud, D., Mayhew, G.F., Rose, D.J., Zhou, S., Schwartz, D.C., Perna, N.T., Mobley, H.L.T., Donnenberg, M.S. and Blattner, F.R. Extensive Mosiac Structure Revealed by the Complete Genome Sequence of Uropathogenic Escherichia coli
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002)
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QSKVLIVEFHQPIAARVLEEAQKLGALPYPVGAESKYEI PPLFYRLSGTFRQANPQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus tag="c4145"
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coli 0157:H7 ortholog: z4730"
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/function="putative transport"
/note="Escherichia coli K-12 ortholog: b3377"
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/protein id="AAN82585.1"
/db_xref="G1:26110400"
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/mol type="genomic DNA"
/strain="CFT073"
/db_xref="taxon:199310"
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/locus_tag="c4147"
complement(1529. .2833)
/gene="yhfT"
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157. .324
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/db xref="GI:13363699"
/translation="MLLLAGKRPYNPCNSFPISGSIMSATDRYSHQ:LYATVRQRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIAQGVYQAQQQIPTENELCTQYNVSRITIRKAISDLVADGVLIRÜGGKGFPVGSQKV
SALLILVSGFTDRGVSQGAKTRKTVLEQBRISARPFCKKLIN TENSESVFHLCRYMYLD
KEPLFIDSSWIPLGSTYDIPDEIYVEGSSTYQLEQBRIDTRVVSDKKTIDIPAATRPQA
KWLKCELGBPLFRISKIAFDQWDKPVHVSELPCRANRITLTIDNKRH"
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ELSMYTQFYDKSARYAENINAGLFOYPVLMAADILLYQTNIVPWGEDQKQHLEISRDI
AQRENALYGDIFKVPEPPIPPIPSGARVMSLLEPTKGASKSDNNRNVIGLLEDPKSVVK
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VADAVSGMLTELQERYHRFRNDEAFLQQVMKDGAEKASAHASRTLKAVYBAIGFVAKP
                                                                                                                                                                                                                                                        /translation="mkTlatigDncVDIYPQINKaFSGGNAVNVAVYCTRYGIKPGCI
TWVGDDDYGTKLKQDLASMGVDISHVHTKHGVTAQTQVBLHDNDRVFGDYTBGVMADF
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99 in 334 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to YHFR ECOLI gi|1789776 percent identity
98 in 265 aa (Conserved in E.coli K-12)"
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Bscheriachia coli CFT073
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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/note="similar to GPH ECOLI gi|1789787 percent identity
in 252 aa (Conserved In E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301660 bp DNA linear BCT 24-DEC-2
Escherichia coli CFT073 section 14 of 18 of the complete genome.
AE016768 AE014075
AE016768.1 GI:26110397
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   Conserved in B.coli K-12)"
                                                                       evidence=not_experimental
transl_table=11
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/gene="ECs4226"
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/gene="BCs4226"
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complement(6616. .7374)
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/gene="ECs4225"
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/gene="ECs4225"
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/transI_table=11
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QAALARERMGLGEVPLIATTALATGVYAVAGFFVAVGYSLSPNPMVAAVLGAVVISA
EVLILREIGKRKGERYSVRNAGSFRANDMLARVALLVGSIFAAIKAAGTTGFSIAV
AIYFLESLGREVQKMAAPVVAVMITGILLAVTATGTFSIAV
COMPIEMERI (2045, .3237)
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/translation="MSFDPTGYTLAHEHLHIDLSGFKNNVDCRLDQYAFICQEMNDLM
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QEMVDETEQZI DGTDLKAGI I AZIGSSBGKI TSLEBKKVFI DAALAHNOTGRETESTHTS
STRMELBQLALLQAHGVDLSRVTVGHCDLKDNLDNI LKMI DLGATVQFDTI GKNSYYP
DEKKLAMLHALRUDGLINRVMLSMDI TRRSHLKANGGYGYDFLLITTF IPQLRQSGFSQ
ADVDVMLRENPSQFFQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="c4149"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ]
Jocus tag="c4150"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (3209. .4087)
/gene="yhfv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="c4150"
complement(4084. .5310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (5311. .6474)
                                                                                                                                                                                                                                                                                                                                                                                                               /locus tag="c4148"
complement (2845, .3237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (4084. .5310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (5311. .6474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="c4151"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon start=1/trans1 table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="yhfv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="yhfW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="yhfw"
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9

gene

80

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LIETARLYGIELYLWTKQFGRNPWIABEKLIALGYSGIVAVDYKEARVWRRAGLPVAHO
GHLVQIPCHQVSDAVEQGTDVITVFTLDKAREISAAVKTGRVQSVLLKVYSDDDFLY
PGQESGFVQHSLHRVYAEIQNIPGHLHAGILHFPCLLMVBEAGGKVLPTPNIHTIVQAR
DQLAKSGIAIEQLANDASCTSLPLLAEYGVTHTEPGHALTGFIPANQCHOPERIA
MLWLSBISHHFRGDSYCXGGGYYRRGHAQHALVFTPRNQKITGFIPANGCHOPERIA
PLAGEHPVSSAVVLCFRTQIFITRSDVVLVSGIHHGEPRIVGRYDSLGNPLEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MGNRANPYTKRKASDMETRINLECDAGVIDKDICKGMMQVVNVLE
TECHLPARSEGGTMAMTHMASALMRSRRGEEIEPLDDELLAELAGSSHWQAVVQLHQV
LLKEFALEVNPCEEGYILAANIYGLWRAANEEV"

/gentempt (6937. ,7785)
/locus tag="c4153"
/locus tag="c4153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
Eukaryotailus
Eukaryotai, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
I. (hases 1 to 90650)
Endrizzi, M.G., Hadinoto, V., Growney, J.D., Miller, W. and
Dietrich, W.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="c4152"
/note="Escherichia coli K-12 ortholog: b3382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus tag="c4153"
/note="Escherichia coli K-12 ortholog: b3383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.6%; Score 33; DB 1; Length 301660; llarity 87.8%; Pred. No. 0.26; Conservative 0; Mismatches 5; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic sequence analysis of the mouse Naip gene array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151285 CTACACTTACATATTCGTTAAACCATATGTGTTTTTGACTT 151325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CIGCACITACACATICGITAAGICATATATGITTTTGACTT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon start=1
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/gene="yhfY"
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complement(8003. .9007)
                                                                                                                                                                                                                                                                                                                          complement (6558. .6962)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (8003. .9007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="trps"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF242432.1 GI:9082149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP242432
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/product = neuronal apoptosis inhibitory protein 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVKLIONSPNIHVPHLKCDFLSNCDSLAAVLASCKKILREIBESGRCFFRAPFYNILDN
FISLKTLINIJSQCPDKETSERFAQALGSLRNLBEILVPTGDGIHQYAKLITRQCLQL
PRICATLATILDNDSVIBIRAVATSGGFQKLEKLDLSMUHKITBEGTRNFCPALDNI
PNICATLNICKHIPEGTQVQATTVKALGQCVSRLPSLTRLHMLSWLLDEBDMKVINDVK
BRHFQSKRLIIFWKWIVPFSPVVLE"
                                                                                                                                   2 (bases 1 to 90650)
Dietrich, W.F.
Dietrich, W.F.
Submitsed (08-MAR-2000) Genetics, HHMI/Harvard Medical School, 200
Longwood Avenue, Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: Naip, rs 7"

/note="synonym: Naip, rs 7"

complement (join (6546. 7941,9650. .9814,12413. .12499,

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27914. .27955,31151. .31256,31944. .32063,35161. .35212,

36038. .36119,42341. .42440,42892. .43462,45016. .45057,

51508. .51891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacobson (1972)

/ gene="Naipl"
/ product="neuronal apoptosis inhibitory protein 1"
/ product="neuronal apoptosis inhibitory protein 1"
complement (join/577, 7941, 9650, .9814, 124131. .1249),
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36038. .36119, 42341. .42440, 42892. .43459)}
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Genome Res. 10 (8), 1095-1102 (2000)
20414747
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                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6546. .51581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="D13Die31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31849. .32057
/mote="D13Die3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Gtf2h2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="Naip1"
                                                                                                   10958627
                                                      MEDLINE
PUBMED
                                                                                                                                   REFERENCE
AUTHORS
TITLE
         JOURNAL
                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Charata, B., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Callins, S., Collymore, A., Cook, A., Cooke, P., Perreira, P., Fitzhay, W., Gage, D., Galagan, J., Gardyna, S., Gorde, S., Gordette, M., Graham, L., Grand, P. Erre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landera, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Macdenald, P., McKernan, K., Mardhia, J., Meneus, L., Maclean, C., Macdonald, P., McKernan, K., Marduim, J., Meneus, L., Norman, C., M., Murphy, T., Naylor, J., Mayuyen, C., Nicol, R., Norban, C., Retta, R., Rieback, M., Rieback, M., Pollara, V., Raymond, C., Retta, R., Rieback, M., Rieback, R., Schuer, S., Schupback, R., Seman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramainan, A., Tavars, N., Travers, M., Travers, M., Travers, M., Travers, M., Travers, N., Tragilio, J., Vesniliev, H., Viel, R., Wo, A., Wilson, B., Wy, Myman, D., Ye, W.J., Young, G.,
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626me="Gatfizh2" .87892,88202. .88279,88879. .>88844}},

fproduct="general transcription factor IIH polypeptide 2" complement (join(67642. .67761,69615. .6964,75206. .75308,7581. .87947,77928. .77991,79262. .79369,79726. .793813,7934. .80024,41662. .81767,84790. .84844,85193. .85433,8756. .87655,87856. .87892,88202. .88279,88789. .88844)}

fpene="gatfizh2" .844; coding region based on similarity to Homo sapiens; may contain additional exons not included
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHTSREVLIIPSSLTTCDPSNIYDLIKTLKTAKIRVSVIGLSAEVRVCTVLÄRETGGT
YHVILDETHYKELLAHHVSPPASSSSECSLIRMGEPQHTIASLSDQDAKPSFEMAHL
INNSTEPGITLGGYFCPQCRAKYCELPVECKICGLTLVSAPHLARSYHHLFPLDAPQE
ISLEEYKGERPCYGCQGELKDQHVYVCTVCQNVPCTDDVPVHDSLHCCPGCIHKIPP
PSGI"
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Mus musculus clone RP23-29L19, WORKING DRAFT SEQUENCE, 8 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="general transcription factor IIH polypeptide 2"
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/db_xref="GI:9082152"
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Birren, B., Nusbaum, C. and Lander, B.
Mus musculus, clone RP23-29119
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HTG: HTGS PHASE2; HTGS DRAI
Mus musculus (house mouse)
Mus musculus
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* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be preserved.

* This sequence will be preserved.

* A 86971: contig of 86971 bp in length 86972 87071: gap of 100 bp 87072 88053: contig of 892 bp in length 88054 88153: gap of 100 bp 99344 99343: contig of 7834 bp in length 98277: contig of 6873 bp in length 98277: contig of 6873 bp in length 98278 105014: contig of 6873 bp in length 98277: contig of 6873 bp in length 98277: contig of 6873 bp in length 98278 105014: contig of 6873 bp in length 195014: gap of 100 bp 19518: losi14: gap of 100 bp 19518: losi15: contig of 14178 bp in length 19592: contig of 160 bp 19518: losi14: gap of 100 bp 19518: losi14: gap of 100
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AC090511 88013 bp DNA linear PRI 14-JUN-2001
Homo sapiens chromosome 15 clone CTD-237008 map 15q21.3, complete
sequence.
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Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Blocm, S., Dors, M., Dickhoff, R., Pleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Traicoff, R. and Hood, L.

Direct Submission

Submitted (27-FEB-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NB, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R., Pate,D. and Hood,L.
Direct Submission
Submitted (14-JUN-2001) Multimegabase Sequencing Center, Institute
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I (bases I to 80013)

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Sequencing of human chromosome 15 D15S146-D15S117 region
Unpublished
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1933 186963: contig of 67571 bp in length 6964 187063: gap of 100 bp 7064 198631: contig of 11568 bp in length. Location/Qualifiers 1..198631 /organism="Mus musculus" /mol_type="genomic DNA" /mb Xref="taxon:10090" /clone="RP23-2919" /clone="RP23-2919" /clone="RP23-2919" /clone="RP23-2919" /clone="RP23-2919" /clone="assembly_fragment clone and:8671 /clone=massembly_fragment clone end:8671 /clone=massembl
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Homo sapiens chromosome 5 clone RP11-224A9, complete sequence.
AC091915
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/clone="Ib="Cal Tech human BAC library D"
/note="This clone overlaps RP11-323F24 AC010999,
/note="This clone overlaps RP11-3597A AC010999,
/note="This clone overlaps RP11-3597A AC010532. Data from these BACs were added and the consensus sequence determined from CTD-237008 to the
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Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
   Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
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1 (bases 1 to 150965)
DS Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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               98105, USA
On Jun 14, 2001 this sequence version replaced gi:13399359
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                                                                                                         59.5%; Score 25; DB 9; Length 88013; 75.6%; Pred. No. 1.5e+02;

    .25594
/note="overlap with RP11-323F24 AC010999"

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/note="overlap with RP11-325L11 AC090532"
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                                                Center: Multimegabase Sequencing Center
Center code: UWMSC
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DOE Joint Genome Institute.
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Search completed: May 26, 2004, 17:22:12 Job time : 591.231 secs

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GenCore version 5.1.6
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Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	May 26, 2004, 15:20:44; Search time 556.41 Seconds (without alignments) 3115.905 Million cell updates/sec	US-10-676-299-6 re: 40 l taagtcaaaaacatatatgacttaacgaatgtgtaagtgc 40
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	OM nucleic -	Run on:	Title: Perfect score: Sequence:

6940544 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Scoring table: IDENTITY\_NUC Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Searched:

GenEmbl:\* Database :

99° ba: \*
90° ba: \*
90° om: \*

em\_sy:\* em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\* em\_ro:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Direct Submission

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Submitted (13-0CT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NGGRS). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borddovsky, Georgia Institute of Technology, Atlanta, GA, 30:32 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG
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Escherichia coli K12 MG1655 section 316 of 400 of the complete
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Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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Bscherichia coli K12
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacee; Escherichia.
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Submitted (16-JAM-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecol@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
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Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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100.0%; Pred. No. 0.0022;
tive 0; Mismatches 0; Indels
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Blattner, F.R.
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Matches 40; Conservative
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J. Bacteriol. 177 (8), 2050-2056 (1995)
95238276
                                                                                                                                 Diorio,C.
Direct Submission
Submitted (06-JUL-1994) C. Diorio, McGill University, 3775
University Street, Montreal, Quebec, H3A 2B4, CANADA
University Street, Montreal, Quebec, H3A 2B4, CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="membrane-located arsenite efflux pump"
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Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CSGC) detabase at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Neb site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; pronotation updates: updated gene identifications and products: pronotation updates: updated gene identifications and products. pronotation in seignements courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'D' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="£250; 100 pct identical to 218 amino acids of YHIQ ECOLI 5W: P37633 but has 32 additional N-ter residues; grg start, alternate starts possible" codon start=1 codon start=1 /transI_table=11 /product="not", hypothetical protein" protein id="AAC76522.1" /protein id="AAC76522.1" /db xref="GI:1789912" /db
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function="orf; Unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="orf, hypothetical protein"
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                                                                                                                                                                                                                              complement (2332. .2727)
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                                                                                                                                                                                                                                                                                                                                                                          'gene="insB"
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Bucteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.

Enterobacteriaceae, Shigella.

I (bases 1 to 11524)

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I (bases 1 to 1000, J. Wang, Y., Shen, Y., Lu, W.C., Wang, J.H., Li, H., T., T., Yang, J., Yang, R., Chu, B., Zhang, X.B., Zhang, J.Y., Yang, G.W., Ku, H., T., Dong, J., Yao, Z.J., Heb. B.K., Chen, R.S., Ma, D.L., Cang, B.Q., Wen, Y.W., Hou, Y.D. and Yu, J.

Genome sequence of Shigella flexmeri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli Nil and O157

INCLEA Acids Res. 30 (20), 4432-4441 (2002)
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FALPALPERVAVVGAGYIAVELAGVINGIGAAKTHLFVRKHAPERSFDPMISETIVEWM
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coli 0157:H7 ref: NP_312399.1"
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AE015361.1 GI:24
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Best Local S:
Matches 40
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AE015361/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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CDS

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AC145934 119941 bp DNA linear HTG 01-AUG-2003 Gallus gallus chromosome UNK clone CH261-4211, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae, Gallus.

1 (bases I to 179941)
Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson,R.K.
Direct Submission
Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                        ö
                Length 11524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1176: contig of 1176 bp in length
1256: gap of unknown length
2558: contig of 1295 bp in length
2558: contig of 1190 bp in length
3948: contig of 1190 bp in length
3948: contig of 1190 bp in length
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7599: gap of unknown length
7591: gap of unknown length
                100.0%; Score 40; DB 1; Length 11 100.0%; Pred. No. 0.0018; Live 0; Mismatches 0; Indels
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of 1456 bp in length
unknown length
of 1459 bp in length
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of 1215 bp in length
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of 1268 bp in length
                                                                                                               2253 TAAGTCAAAACATATATGACTTAAGGAATGTGTAAGTGC 2214
                                                                                            40
                                                                                            1 TAAGTCAAAACATATATGACTTAACGAATGTGTAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of Gallus gallus clone
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                                                                                                                                                                                                                                                                                            AC145934
AC145934.1 GI:33386884
                                                                                                                                                                                                                                                                                                                                HTG; HTGS PHASE1.
Gallus gallus (chicken)
Gallus gallus
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Ouery Match
Best Local Similarity 100..
Loca 40; Conservative
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1277
2559
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12038
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AC145934
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| 15386 | 17945 | 17946 | 1859 | 19 | 1898 | 17946 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 19948 | 1
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Gaps ö Query Match
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PEATURES

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note="CG Site No. 17791; membrane protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="sn-Glycerol-3-phosphate transport system"
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                                          complement (1085. .1112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ugpQ"
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                                                                                                            complement (1146.
                                                                                                                                                                              complement (1181.
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                                                                                     note="43
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PISGDYRGYQVYSMPPPSSGGGIHIVOILNILENPDMKKYGFGSADAMQIMAEABKYAY
ADRSEYLGDPDFVKVPWQALTNKAYAKS"
                                                                                                                                                                                  BCT 07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award #G00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps and conflicts with other sequence determinations are annotated. The start of this entry overlaps the start of the entry ECUM82 (L10328) by $47 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dub_errain="MG1655"
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/db_xref="taxon:562"
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EC27-334, EC30K606A-14, EC30K606A-12, EC30-154, EC27-385,
EC27-1129, EC30MM9, EC37-239, EC30MM3, EC27-87955,
EC18-200, EC27-1135, EC30R3900-8B, EC30R3900-5B, EC19MM6,
subcloning"
                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-MAR-1994) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysis of the Escherichia coli genome. V. DNA sequence of region from 76.0 to 81.5 minutes
Nucleic Acids Res. 22 (13), 2576-2586 (1994)
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complement(<1. .1085)
/gene="ggt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 225419)
Sofia,H.J., Burland,V., Daniels,D.L., Plunkett,G. III and
Blattner,F.R.
                                                                                                                                                                              DNA linear B
76.0 to 81.5 minutes.
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/note="corresponds to lambda clone BCi9-98"
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132260 TAAGTCAAAACATATATGACTTAACGAATGTGTAAGTGC 132299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Escherichia coli"
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/strain="K-12"
                                                                                                                                                                          ECCOUNT6 225419 bp
E. coli chromosomal region from
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/transl_table=
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                                                                                                                                                                                                                                                                                          U00039.1 GI:466582
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COMMENT

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PROGRESS ***, 6 unordered pieces.
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LVVMLVYAFFTDTFPYTDATGGGPVQATFTLIYKIYRBGFTGLDLASSAAQSVVLMFF
VIVLTVVQFRYVESKVRYQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQRFNAENPDYKIVPTYKGNYEQNLSAGIAAFRIGNAPALLQVYEVGTATMMASKAIK
PVYDVPKEAGIQEDBSQFVPTVSGYYSDSKTGHLLSQPFNSSTPVLYYNXDAFKKAGL
DPBQPPKTWQDLADYAAKLKASGMKCGYASGWQGWIQLENFSAMNGLPPASKNNGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDAVLEFNKPEQVKHIAMLEEMNKKGDPSYVGRKDESTEKFYNGDCAMTTASSGSLAN
TEXTAKEVYGVGWPYDADADADADANJA IGGABLWWQGGONEETYTGVAKFLDFLAKP
ENAAEWHOKTGYLD FITKAAYDLTREGGFYEKNPGADTATRQMLAKPPLPFTKGLRLGN
MPQIRVIVDEELESVWTGKKTPQQALDTAVERGNQLLRRFEKSTKS"
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fetandard_name="RBP; repetitive extragenic palindromic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="mRNA start determined by S1 mapping; Molecular Microbiol. 2:767 (1988)" /evidence=experimental
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complement(4286. .5173)
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/function="ng-dycerol-3-phosphate transport system"
/note="CG Site No. 40"
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function="an-Glycerol-3-phosphate transport system"
/note="CG Site No. 39; periplasmic binding protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6618. .15331)
/note="corresponds to J05516; ECOLIVHMGF(1. .8703)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 40; DB 1; Length 225419; Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 40; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="CG in J05516; GC in X13141 and here"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6845. .6846
/note="C in J05516; CC in X13141 and here"
complement (6986. .7711)
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/note="GGCG in X13141; SSGS here"
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/note="GC in X13141; SS here"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (6651, .6679)
/note="includes pho box"
complement (6695, .6723)
                                                                                                                                                                                                                                                                                                                         complement (5271, ,6587)
/gene="ugpB"
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complement (4286. .5173)
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AC146183.2 GI:38154191
HTG; HTGS PHASE1.
HTG; HTGS PHASE1.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                              Wilson,R.K.
Direct Submission
Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 242495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
On Nov 4, 2003 this sequence version replaced gi:33387136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 1369: contig of 1269 bp in length
270 1369: gap of unknown length
370 2935: contig of 1566 bp in length
373 3035: gap of unknown length
374 4616: contig of 1581 bp in length
4716: gap of unknown length
577 6291: contig of 1575 bp in length
578 6391: gap of unknown length
579 8254: contig of 1863 bp in length
570 8354: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Mi3; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer BT; 0% of reads
Chemistry: Dye-primer BT; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least Q40
Consensus quality: bases at least Q40
Consensus quality: bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .370. .2935
'note≈"assembly_name:Contigl3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6392. .8254
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8355. .242495
/note="assembly_name:Contig20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="assembly_name:Contig12"
1370. .2935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="assembly_name:Contig14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_name:Contig18"
                                                                                                                                                                                                                                                         The sequence of Pan troglodytes clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .242495
/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DN/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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ORIGIN

AC146183 242495 bp DNA linear HTG 04-NOV-2003 Pan troglodytes chromosome y clone CH251-548L16, \*\*\* SEQUENCING IN

RESULT 6
AC146183/c
LOCUS
DEFINITION

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AQRVHFFFFRNGGSPVVDRNALIAALQXGRIHAAGLLUVFBCBFLSTHTLF
GAEGPAXMKSSAIFINAGGSVVDBNALIAALQXGRIHAAGLUVFBCBFLSVDSFLLS
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VMVGDYIAQQGTQVSFVANGIQFPTSQQASBYNKLIAPLAADAQPILPAGMTTAVTATQ
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B3552"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=*residues 21 to 759 of 759 are 98.78 pct identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="enzyme; Biosynthesis of cofactors, carriers:
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complement(3293. .3919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (2215. .3189)
                                                                                                                                                               Tocus tag="S4181"
335. 2165
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4160. .6439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="ylaE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="yiaD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="yiaD"
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Shigella flexmeri 2a str. 2457T section 15 of 16 of the complete
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activator of has"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus teg="S4180"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shigella flexneri 2a str. 2457T
Shigella flexneri 2a str. 2457T
Shigella flexneri 2a str. 2457T
Bacteria Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.

(bases 1 to 289816)
May L., Goldbergi, M. B., Burland, V., Venkatesan, M.M., Deng, W.,
Fournier, G., Mayhew, G.F., Plunkett, G. III, Rose, D.J., Darling, A.,
Mau, B., Perna, N.T., Payne, S.M., Runyen-Janecky, L.J., Zhou, S.,
Complete Genome Sequence and Comparative Genomics of Shigella
flexneri Serotype 2a Strain 2457T
Infect. Immun. 71 (5), 2775-2786 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 289816)
Weil-J., Gollberg, M.B., Burland, V., Venkatesan, M.M., Deng, W., Feil-J., Gollberg, M.B., P., Plunkett, G. III, Rose, D.J., Darling, A., Mau, B., Perna, N.T., Payne, S.M., Runyen-Janecky, L.J., Zhou, S., Edwartz, D.C. and Blattner, F.R.
Direct Submission
Submitted (13-JUN-2002) Genetics Laboratory, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
1. .289816
                                                                              Gaps
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                    ch 100.0%; Score 40; DB 2; Length 242495; l Similarity 100.0%; Pred. No. 0.0011; 40; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                  40
                                                                                                                               1 TAAGTCAAAAACATATATGACTTAACGAATGTGTAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serotype="2a"
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complement(896. .1021)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (896. .1021)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="S4179"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:30043426
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transI_table=1
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AE016992 AE014073
AE016992.1 GI:30
                                                 Local Similarity
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12704152
                       Query Match
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DEFINITION
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SOURCE
ORGANISM
                                                 Best Loc
Matches
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AUTHORS
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AE016992
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66023 TAAGTCAAAACATATGACTTAACGAATGTGTAAGTGC 66062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67. .1419
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Escherichia coli O157:H7 EDL933
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AE005575 AE005174
AE005575.1 GI:12518196
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AE005575/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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JOURNAL
MEDLINE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="yiac"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon start=1
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complement(6845. .7408)
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7566. .3264
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//inction="putative enzyme, Not classified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Jocus teg="S4186"
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function/modification"
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to residues 1 to 739 of 739 from Escherichia coli K-12
B3551"
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Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 40; Conservative 0; Mismatches 0; Indels 0;
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complement (6408, .6848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (6408. .6848)
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complement(6845..7408)
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1 TAAGTCAAAAACATATAAGACTTAACGAATGTGTAAGTGC 40

ABO05575 11-MAR-2001 Escherichia coli 0157:H7 EDL933 genome, contig 3 of 3, section 194 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriales dammaproteobacteria; Enterobacteriales; Enterobacteriacaae; Escherichia.

Butan, N. T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J. D., Pose, D. J., Mayhew, G. F., Evans, P. S., Gregor, J., Kirkpatrick, H. A., Posfai, C., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grobbeck, E. J., Davis, N. W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T. S., Lin, J., Yen, G., Schwartz, D. C., Genome sequence of enterohaemorrhagic Escherichia coli O157:H7 Nature, 409 (6819), 529-533 (2001) Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Nayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Apodaca, J., Anantharaman, T.S., Dim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, P.R.

Direct Submission Blattner, P.R.
Submitted (12-00T-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Wall, Madison, WI 53706, USA 1. .1107i /organism="Bscherichia coli O157:H7 EDL933" /mol type="genomic DNA" /strāin="EDL933" /note="synonym: Z4903" 2300. .2653 /gene="arsR" 2300. .2653 /gene="arsR" g

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M3165: B3566"

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/note="Residues 1 to 176 of 176 are 99.43 pct identical to
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residues 1 to 176 of 176 from Escherichia coli K-12 Strain
MG1655: B3507"

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Bscherichia coli 0157:H7 DNA, complete genome, section 16/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym: Z4908"
6499, .7098
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/function="membrane; Cell envelop: Outer membrane
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Best Local S:
Matches 37,
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LOCUS
DEFINITION
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| Codon start=| | Codon start=| |
| Cadon start=| | |
| LiansI table=| | | |
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| AAVAALFANGCAALILTIVAFPVILENIAFRANIALITAVARGHALILTVAKRGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGARGATAVANIAGTVARGANACHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGATAVANIAGTVARGANACHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGANACHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALILTGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHALITGVARGHAL
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                                                                                                 117 of 117 are 94.87 pct identical to 117 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sensitivity"
hore="Residues 1 to 141 of 141 are 98.58 pct identical to
residues 1 to 141 of 141 from Escherichia coli K-12 Strain
MG1655: B3503"
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2707. .3996
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residues 1 to 117 of
MG1655: B3501"
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i (sites)
Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S.,
Makino, K., Ishii, K., Hattori, M., Tatsuno, I., Abe, H., Ilda, T.,
Yamamoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T.,
Sasakawa, C. and Shinagawa, H. the prophage VT2-Sakai carrying the
Complete nucleotide sequence of the prophage VT2-Sakai carrying the
verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
derived from the Sakai outbreak
Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shinagawa,H. Complete nucleotide sequence of the prophage VT1-Sakai carrying the Complete nucleotide sequence of the prophagic Escherichia coli O157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
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Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen.info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sites)
Obnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
Hayashi,T.
Comparative analysis of the whole set of rRNA operons between an
enterchemorrhagic Escherichia coli 0157:H7 Sakai strain and an
Escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
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Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
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Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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E.coli K-12)"
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Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,M., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
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151. .318

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                                                                            Escherichia coli 0157:H7
Escherichia coli 0157:H7
     AP002565 BA000007
AP002565.1 GI:13363693
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99 in 462 aa (Conserved in E.coli K-12)"
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3045. 3642.

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3872. .4204
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coli 0157:H7 ortholog: z4730"
1 (bases 1 to 301660)
Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
Extensive Mosiac Structure Revealed by the Complete Genome Sequence Tropathogenic Escherichia coli
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002)
                                                                                                                                                                                                                                                          Roesch, P.,
                                                                                                                                                                                                                          (bases 1 to 301660)
Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J., Stroud,D., Mayhew,G.P., Rose,D.J., Zhou,S., Schwartz,D.C., Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
                                                                                                                                                                                                                                                                                                                                                                                     of
USA
                                                                                                                                                                                                                                                                                                                      Strown, T., Mobley, H.L.I., Lowers and Direct Submission Submitted (20-JUN-2002) Genetics Laboratory, University Wisconsin - Madison, 445 Herry Mall, Madison, WI 53706, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               locus tag="c4146"
note="Escherichia coli K-12 ortholog: b3376"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (1529. .2833)
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  REFERENCE
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                                                                                                                                TITLE
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AE016768 AE014075
                                                                                                                                                                           /trānslation="mkTlatigDncVDIyPQLnkafsggnavnvavycTrygIkPgCI
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ELSRMTQ FKDKSARYARNI NACL PDY PVLMAAD I LLY OTNL VPVGEDOKOHLELSRDI
AQRFNALYGD I FKVPRPPI PKSGARVMS LLEPTKKOAS KSDDNRNAVI GLLEDPKSVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIKRAVTDSDEPPVVRYDVQNKAGVSNLLDILSAVTGQSIPELEKQFEGKAYGHLKGB
VADAVSGMLTELQERYHRFRNDEAFLQQVMKDGAEKASAHASRTLKAVYEAIGFVAKP
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Escherichia coli CFT073
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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complement(6616. .7374)
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AE016768/c
LOCUS
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PQESSGFVQBSLHEVVAEIQMLPGLHLAGLHHPPCLLMDEAAGKVLPPPULHTLVQAR
DQLAKSGI AI PQLNA PASTGSLPLLABYGVTHT PRCHALTGTI PANQQGDQPERIA
MLALSBI SHHFRGDSYCYGGGYRRGHAQHLLVFT PRNQRI TSTYLNAVDDSS IDYTL
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Llkbralevnpceegyllanlyglwmaaneev"
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Mus musculus clone RP24-200D15, WORKING DRAFT SEQUENCE, 3 unordered
LIETARLYGIBLYLMTKQFGRNPWLAEKLLALGYSGIVAVDYKBARVMRRAGLPVAHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 166112)
Birren, B., Nusbaum, C. and Lander, B.
Mus musculus, Chone RP24-200D15
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house moüse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.0%; Score 31.6; DB Best Local Similarity 89.5%; Pred. No. 0.64; Matches 34; Conservative 0; Mismatches
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complement(8003. .9007)
                                                                                                                                          complement (6558. .6962)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (6937. .7785)
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AC102260
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COMPLEMENT (2845. .3237)
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complement(2845. .3237)
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Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, Y., Cooke, P., Dehrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Fareira, P., Pitzhugh, W., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, I., Fulme, M., Iliev, I., Johnson, R., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Merheeters, R., Meldrin, J., Manneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nail, D., O'lover, J., Petta, R., Phurkhang, P., Pierre, N., Pollara, V., Norbu, C., Retta, R., Rieback, M. Riley, R., Schauer, S., Schuback, R., Seman, S., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Tropham, K., Travers, M., Travis, N., Trighlio, J., Vassillev, H., Vol. M., Milley, M., Travis, N., Trighlio, J., Yassillev, H., Viel, R., Willey, M., Travis, N., Trighlio, J., Yassillev, H., Viel, R., Willey, M., Trighlio, J., Yassillev, H., Viel, R., Willey, M., Trighlio, J., Yassillev, H., Sibmitted (Johnson, B., Wix, Waman, D., Ye, W.J., Young, G., Sibmitted (Johnson, B., Miller, A., and Zody, M., Submitted (Johnson, B., Miller, A., and Zody, M., Submitted (Johnson, B.)
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Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 166112)

Birren, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Boguslawkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cooke, P., Corum, B., Dakrellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Paro, S.,

Perreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,

Graham, L., Grand-Fierre, N., Hafez, N., Gardon, G., Hagopian, D., Macdon, K., Kanat, A., Karatas, A., Kalis, C., Landers, T., Levine, R., Jones, C.,

Macdonald, P., Major, J., Manbhitt, R., MacLan, C.,

Macdonald, P., Major, J., Manbhitt, R., MacLan, C.,

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Nguyen, C., Nicol, W., Norbu, C., O'Connor, T., O'Donnell, P.,

Nguyen, C., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,

Wassiliev, H., Venkataraman, V.S., Viel, R., Vora, A., Milson, B., Mu, X.,

Myman, D., Young, G., Zainoun, J., Zembek, L., Zammer, A., and Zody, M.

Blirect Submission
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Insert size: 165912; sum-of-contigs
Quality coverage: 12.6 in Q20 bases; agarose-fp
Quality coverage: 12.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L18273

Center clone name: 200 D 15

Center clone name: 200 D 15

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 165601 bases at least Q40

Consensus quality: 165840 bases at least Q20

Consensus quality: 165883 bases at least Q20
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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COMMENT

\* NOTE: This is a 'working draft' sequence. It currently

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
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Mouse DNA sequence from clone RP23-331M18 on chromosome 4, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

    (bases 1 to 176496)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                        1 37442: contig of 37442 bp in length
3743 37542: gap of 100 bp
37543 101600: contig of 64058 bp in length
101601 101700: gap of 100 bp
101701 166112: contig of 64412 bp in length.
Location/Qualifiers
1. 166112 | Augusti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TAAGTCAAAAACATATATGACTTAACGAATGTGTAAGTG 39
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1 Similarity 76.9%; Pred. No. 1.5e+02;
30; Conservative 0; Mismatches 9;
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101701. .166112
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Contact: humquery@sanger.ac.uk
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Direct Submission
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Best Local Similarity
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us-10-676-299-6.rge

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chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, GANISSPROT: Tr:, TREMBL; Wp:, WORWPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF242431S2
Mus muscults Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gff2h2) genes, complete cds.
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Submitted (08-MAR-2000) Genetics, HHMI/Harvard Medical School, 200
Longwood Avenue, Boston, MA 02115, USA
Location/Qualifiers
1. 90650
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Endrizzi, M.G., Hadinoto, V., Growney, J.D., Miller, W. and Dietrich, W.F.
                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-331M18 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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1. 176496
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Mus musculus
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AF242432.1 GI:9082149
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AF242431S2
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12799, 12941, 21794, 21941, 24127, 26238, 26102, 26759, 27914, 27995, 31161, 31250, 31944, 12413, 135212, 27914, 27995, 31161, 31250, 31944, 12413, 135212, 27914, 27995, 31611, 31250, 31944, 23406, 23616, 23611, 35212, 36038, 36119, 42341, 42440, 42892, 43459))
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GIGIIVTKSKRAEKLTELSGNPRHITTSLKTAVDWTCHGEPSELYNSLSWAMOTLKHWP
GHTSREVLIIFSSLTTCDPSNIYDLIKTLKTAKIRVSVIGLSAEVRVCTVLARETGGT
YHVILDETHYKELLAHVQSPPRASSSSECSIIRWGFPQHTIASLSDQDAKPGFSMAHL
DNNSTEPGLTLGGYFCPQCRAKYCELPVECKICGLTLVSAPHLARSYHHLFPLDAFQB
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complement(join(6546. 7941,9650. .9814,12413. .12499,
12789. .12941,21794. .21961,24127. .26238,26702. .26759,
27914. .27995,31151. .31250,31944. .32063,35161. .35212,
36038. .36119,42341. .42440,42892. .43462,45016. .45057,
/gene="Naip1"
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/gene="Gtf2h2"
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/note="D13Die3"
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Zembek, L., Zimmer, A. and Zody, N.
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AC091691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listen, B., Linton, L., Nusbaum, C., Lander, B., Ali, A., Allen, M., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S. Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Oraham, L., Gardyna, S., Gord, S., Goyette, M., Oraham, L., Gardyna, S., Landzers, M., Karatas, A., Karatas, A., Karatas, A., Karatas, A., Karatas, M., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kals, C., Lakoque, K., Lamazares, R., Landzers, R., Landzers, R., Johnson, R., McCerthy, M., McDwan, P., McKernan, K., Marquis, N., Matthews, C., McCarthy, M., McDwan, P., McKernan, K., Marquis, N., Matthews, C., Micol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Stubramanian, A., Talamas, J., Teefaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wam, D., Ye, W., J., Young, G., Laine, Shamisten, M., Raver, A., Wilson, B., Wu, X., Wam, D., Ye, W., J., Young, G., Shamer, S., Shamer, S., Schupback, E., Zammer, A., Tertini, D., Ye, W.J., Young, G., Shamer, S., Schube, L., Zammer, A., Tertini, D., Ye, W.J., Young, G., Shamer, S., Shamer, S., Schupback, D., Young, G., Shamer, S., Shamer, S., Sancos, B., Wu, X., Wam, J., Young, G., Shamer, S., Schupback, E., Zamer, A., Wassiliev, H., Sahmer, A., Sancos, B., Wu, X., Wam, J., Young, G., Shamer, S., Schupback, E., Zamer, A., Sancos, J., Wassiliev, M., Sancos, J., Wassiliev, M., Sancos, S., Sancos, 
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Biren,B., Nusbawn,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,I., Boukhgalter,B., Camarata,J., Chang,J., Charara,B., Chepel,Y., Collymore,A., Cooke,P., Dekrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,J., Johnson,R., Matthews,C., Kararas,A., Kells,C., Ianders,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Mihova,T., Manga,V., McZatthy,M., Meldrim,J., Meneus,L., Mihova,T., Merga,V., Marphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C., Phunkhang,P., Pierre,M., Saymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange,Thosan,M., Viel,R., Vo,A., Wilson,B., Wu,X., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
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I SLEEYKGER FCYGCQGELKDQHVYVCTVCQNVFCVDCDVFVHDSLHCCPGCIHKI PT
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1 (bases 1 to 156569)
Birren, B.; Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-912D18
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Homo sapiens chromosome 18 clone RP11-912D18 map 18, 2 ordered
                                                                                                                                                                                                                          Gaps
                                                                                                                                        Score 24.2; DB 10; Length 90650;
Pred. No. 2.2e+02;
0; Mismatches 8; Indels 0;
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HTG; HTGS PHASE2; HTGS_TULTOP; HTGS_CANCELLED.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                66076 AGTCAATAATATGTGTATAAACAAATGTATAAGTG 66112
                                                                                                                                                                                                                                                                                         3 AGTCAAAAACATATATGACTTAACGAATGTGTAAGTG 39
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                                                                                                                                        60.5%;
ilarity 78.4%;
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Best Local Similarity
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AC091691 164314 bp DNA linear PRI 01-MAY-2002
Homo sapiens chromosome 18, clone RP11-47G4, complete sequence
AC091691
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              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi; Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I tases 1 to 164314)
Birren, B., Linton, L., Musbaum, C. and Lander, B.
Homo sapiens chromosome 18, clone RP11-47G4
                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as tuns of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 19479 99578: Gontig of 99478 bp in length

* 99579 156569: contig of 56991 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.5%; Score 24.2; DB 2; Length 156569; 78.4%; Pred. No. 2e+02; ive 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                         77310 AAGTCAAAAACATGTATTATTTAAGTAATTTCTAAAT 77346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-912D18"
/clone lib="RPCI-11 Human Male BAC"
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol type="genomic DNA"
/db xref="taxon:9606"
/chromosome="18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 78.4
Matches 29, Conservative
Direct Submission
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Center: Whitehead Institute/ MIT Center for Genome Research
                                      /clone lib="RPCI-11 Human Male BAC" 635. .675
/rpt_family="(CA)n" 828. .2491
/rpt_family="L2" 2607. .2639
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ement(1601)
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. 13024
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"LIPA3"
233
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opt family="MLTIC"
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omplement (14954. .15101)
rpt family="MRR67C"
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/rpt family="L1MD2"
20225. .20249
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6988_ .7010
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/db_xref="taxon:9606"
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6086. .6139
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complement(7011. 7047)
/rpt_family="LiPA7"
complement(7048. 10232
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2650. .2702
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/rpt_family="Ricksha"
2696. .3085
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complement(3162. .6089
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family="Ricksha"
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complement(16290.
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complement(22445.
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family="L2"
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Direct Submission

Direct Submission

Burnetted (18-MY-2011) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 164314)

Birren, B. Linton, L., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chagalter, B., Erown, A., Camarate, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Perreira P., FitzHugh, W., Gago, D., Galagan, J., Gardyna, S., Ginde, S., Govette, M., Graham, L., Grand Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, J., Karat, A., Kalls, C., LaRocque, K., Landarares, R., Landers, T., Lehoczky, J., Levine, R., Inhoblad-Toh, K., Isu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarth, W., McCarth, W., McCarth, W., McCarth, W., McCarth, W., McCarth, Y., Murph, T., Wallor, J., Mouyen, C., Nordan, C., Norman, C.H., O'Connor, T., O'Domell, P., O'Nai, D., Oliver, J., Petersen, K., Phunkhang, P., Pierre, N., Pollara, V., Raymord, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Stenaer, S., Severty, P., Spencer, B., Stanger-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Shaite, M., Santos, M., Stofauer, S., Severt, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Shaite, M., Santos, M., Marph, A., Santos, M., Stofauer, S., Severt, W., Stofauer, S., Severt, M., Stofauer, S., Severt, W., Stofauer, S., Severt, W., Stofauer, S., Severt, M., Stofauer, S., Severt, M., Stofauer, S., Severt, M., Stofauer, S., Severt, M., Stofauer, S., Severt, S., Shaite, M., Stofauer, S., Severt, M., Stofauer, S., Severt, M., Stofauer, S., Severt, S., Santos,
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Submitted (14-2RP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Brom, R., Camarata, J., Campoplano, A., Chang, J., Chargelo, W., Calinus, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Terreira, P., Pitzhugh, W., Gagel, D., Galagan, J., Gardyna, S., Ginde, S., Govette, M., Graham, L., Grand Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamar, A., Karatas, A., Lancora, E., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Mienga, V., Murphy, P., Pierre, N., Pollyer, D., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Deterson, R., Phukhana, P., Petre, R., Polyson, C., Rette, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Spencer, B., Stanger, There, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Lainnon, J., Zembek, L., Zimmer, A. and Zody, M., Tanish, J., Tanish,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCarthy, M., Marchan, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Mguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierra, N., Pollara, V., Raymond, C., Retta, R., Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougenez, C., Spencer, B., Stange-Thomann, M., Travis, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Young, G., Direct Submission
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Query Match 60.5%; Score 24.2; DB 9; Length 164314; Best Local Similarity 78.4%; Pred. No. 2e+02; Matches 29; Conservative 0; Mismatches 8; Indels 0;

Search completed: May 26, 2004, 17:22:16 Job time : 560.41 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

May 26, 2004, 15:20:44; Search 1:10:10:10:10:10:10:10:10:10:10:10:10:10	OM nucleic - nucl	nucleic search, using sw model
score: 23 table: 1Ltaatcatatgcgtttttggtta 23 table: 1DENTITY NUC dapop 10.0, Gapext 1.0  1: 3470272 seqs, 21671516995 residues  In day at a satisfying chosen parameters:  DB seq length: 200000000  DB seq length: 200000000  DB seq length: 200000000  DE seq length: 200000000  DE seq length: 200000000  DE seq length: 200000000  DE seq length: 45 summaries  GenEmbl:*  1: 9D ba:*  1: 9D ba:*  2: 9D lengt:*  1: 9D ba:*  1: 9D ba:*  2: 9D lengt:*  2: 9D lengt:*  1: 9D ba:*  1: 9D ba:*  1: 9D ba:*  1: 9D lengt:*  2: 9D lengt:*  2: 9D lengt:*  1: 9D lengt:*  2: 9D lengt:*  3: 9D lengt:*  3: 9D lengt:*  4: 9D lengt:*  2: 9D lengt:*  3: 9D lengt:*  3: 9D lengt:*  4: 9D lengt:*  3: 9D lengt:*  3: 9D lengt:*  4: 9D lengt:*  3: 9D lengt:*  3: 9D lengt:*  4: 9D lengt:*  3: 9D lengt:*  4: 9D lengt:*  3: 9D	: uo	26, 2004, 15:20:44 ; Search time 319.936 Secc [without alignments] 3115.905 Million cell
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/note="unnamed protein product; ArsR protein (AA 1 - 117)"
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R64 DNA, complete sequence.
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                                                                                                                                                                                                                                         Direct Submission
Submitted (09-AUG-1989) Rosen B.P., Department of Biochemistry,
Wayne State University, School of Medicine, 54- E Canfield Avenue,
Detroit MI 48201, U S A
Location/Qualifiers
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Identification of the metalloregulatory element of the plasmid-encoded arsenical resistance operon Nucleic Acids Res. 18 (3), 619-624 (1990)
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Shufflon: multi-inversion of four contiguous DNA
plasmid R64 creates seven different open reading
Nucleic Acids Res. 15 (3), 1165-1172 (1987)
3029698
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/note="pot. ribosome binding site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Escherichia coli"
/mol rype="genomic DNA"
/db xref="taxon:562"
/clone="pWSU1"
/clone="pWSU1"
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/clone="pwsu2"
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/note="pot. -10 region"
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Puruya,N. and Komano,T.
Determination of the nick site at oriT of Incll plasmid R64: global
similarity of oriT structures of Incll and IncP plasmids
J. Bacteriol. 173 (20), 6612-6617 (1991)
1917882
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Nucleotide sequence and characterization of the traABCD region of Incll plasmid R64
J. Bacteriol. 175 (16), 5035-5042 (1993)
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Purification and characterization of thin pili of Incl1 plasmids Collb-P9 and R64: formation of PilV-specific cell aggregates by type IV pill
J. Bacteriol. 180 (11), 2842-2848 (1998)
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lasmid 32 (1), 80-84 (1994)
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Requirement of a limited segment of the sog gene for plasmid R64
conjugation
Plasmid 38 (1), 1-11 (1997)
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                   Komano, T., Toyoshima, A., Morita, K. and Nisioka, T.
Clohing and nucleotide sequence of the oriT region of the Incli
plasmid R64
J. Bacteriol. 170 (9), 4385-4387 (1988)
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Nuclectide sequence and characterization of the trbABC region the Incil Plasmid R64: existence of the pnd gene for plasmid maintenance within the transfer region J. Bacteriol. 178 (6), 1491-1497 (1996)
8626273
                                                                                                                                      Furuya, N., Nisioka, T. and Komano, T.
Nucleotide sequence and functions of the oriT operon in Incliplasmid R64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The plasmid R64 thin pilus identified as a type IV pilus J. Bacteriol. 179 (11), 3594-3603 (1997) 9731521 9971605
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Genet. 213 (1), 30-35 (1988)

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/protein_id="BAB91569.1"
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/translation="WLQLFPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQ
PKISRHLAMLRESGILLDRKQGKWVHYRLSPHIPSWAAQIIEQAMLSQQDDVQVIARK
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RFWLAQQPMSFVQNEKVKAFIZASGABGLPLLLLDGETVMAGRYPKRAELARWFGIPL
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join(1598. .4147,20047. .20832)
/insertion geq="IS2"
complement[join(3609. .4147,20047. .20418)]
/gene="yadA"
join(4188. .7818,18208. .20046)
/note="different from Tin5393[gb:M96392] in IS1133 insert position and terminal direct repeat"
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Submitted (17-OCT-2003) Wellcome Trust Sanger Institute, Hinxton, cambridgeshire, CB10 1SA, UK. B-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 18, 2003 this sequence version replaced gi:35208834.
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Actinopcerygii; Neoperygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 Chases 1 to 176325)
                                                                                                                                                                                                                                                      /note="99 pct identical to sp:ARD1_ECOL1,sp:P46003[ArsD_plasmid R773]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="99 pct identical to pir:A25937[ArsA of plasmid R773, arsenical pump-driving AFPase]
location 3593. .3597 and location 20833. .20837 are
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HTG: HTGS: PHASE1; HTGS: DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
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Chemistry: Dye-terminator; 100% of reads
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/gene="arsA"
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/gene="arsD"
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Location/Qualifiers
1.-12086
| Corganism="Salmonella typhimurium" | Mol_type="Genomic DNA" | Mol_type="Genomic Complement (join(20047. 2018) are dupulicated" | Mol_type="Genomic Complement (4143. 4147) and location complement (4143. 4147) are dupulicated" | Mol_type="Genomic Complement (4143. 4147) and location complement (4143. 4147) are dupulicated" | Mol_type="Genomic Complement (4143. 4147) are dupulicated" | Moltype="Genomic Complement (4143. 4147) | Moltype="Genomic Complement (4143. 4147) | Moltype="Genomic Complement (4143. 4147) | Moltype="Genomic Complement (
                                                                                                                                                                                                                                                                                  Sampei,G., Komano,T., Sasaki,T., Tachibana,K., Furuya,N., Saito,Y.,
Suzuki,T. and Mizobuchi,K.
Coganization and diversification of plasmid genomes: complete
nucleotide sequence of R64 genome
Unpublished
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HPPYVOKRTFVGRKYAFRPRKORLLDALWPVLVSFSDAGTHTVGMSVTRLAEEISPKD
SEGHVIPELEVTVSRLSRLLAEQVRFGVLGVSEETMWDREHRORLPRYWITPAGWOM
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REKAAASKRANRLKKLPVDQQIYEMAEYLRKRLPPDBAYPCSDDHLKRLAIRBLRQLB
LTLAAPPPH"
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                                                                             Komano,T., Yoshida,T., Narahara,K. and Furuya,N.
The transfer region of Incll plasmid R64: similarities between R64
tra and legionella icm/dot genes
Moi. Microbiol. 35 (6), 1348-1359 (2000)
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/gene="arest"
2761. 3114
/gene="arest"
/note="100 pct identical to sp:ARR1_ECOL1, sp:P15905[ArsR
/codon_start=1
/codon_start=1
/transI_table=11
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/gene="repy"
/note="100 pct identical to pir:A35445[Repy of plasmid
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/translation="MKPYQRFNPYQCINTRHNRSAISDSLWQV"
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/gene="repz"
455. .1486
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Sampei, G. and Mizo
Direct Submission
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Center: Wellcome Trust Sanger Institute
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Zebrafish DNA sequence from clone DKBY-73N10 in linkage group 18,
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Submitted (06-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
zfish-helpssanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 31, 2003 this sequence version replaced gi:37936371.
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Actinopterygii, Neopterygii, Teleostei; Ostariophysi; 
Cypriniformes; Cyprinidae; Danio.
Consensus quality: 175000 bases at least Q40 Consensus quality: 175423 bases at least Q30 Consensus quality: 175742 bases at least Q30 Consensus quality: 175704 bases at least Q20 Insert size: 176025; sum-of-contigs roser size: 185227; 44,4 error; agarose-fp Quality coverage: 10.83x in Q20 bases; sum-of-contigs Quality coverage: 10.36x in Q20 bases; agarose-fp
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                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1109 68208: gap of 100 bp
1209 72158: contig of 3950 bp in length
1259 72258: gap of 100 bp
1259 158147: contig of 85889 bp in length
148 158247: gap of 100 bp
100 contig of 18078 bp in length.
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/clone lib="CHOR1-21"

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clone=end:77
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158248. .176325
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

En: EMBL: Sw: SWISSEROI; Tr: TREMBL: Wp:, WORNPEP information on the WORWERP database can be found at hittp://www.sanger.ac.ubclones occasionally display incomsistency over the length of monouncleotide AT runs and conserved TA repeats. Where this is found the longest good quality representation will be admited.
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Zebrafish DNA sequence from clone CH211-208D15 in linkage group 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-73N10
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Strinopterygii, Neopterygii, Teleostel; Ostariophysi,
Cypriniformes, Cyprinidae, Danio.

    (Dases 1 to 215891)

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zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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Submitted (20-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
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100.0%; Pred. No. 3.5e+02;
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Web site: http://www.sanger.ac.uk
                                    Contact: zfish-help@sanger.ac.uk
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AL928692
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us-10-676-299-7.rge

COMMENT

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BX571883 253172 bp DNA linear VRT 23-SEP-2003
Zebrafish DNA sequence from clone DKEY-151P17 in linkage group 18,
complete sequence.
BX571883
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 253172)
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Contect project Information
Cener project name: 2c22301
Cener project name: 2c22301
Cener project name: XGAP4; version
Assembly program: XGAP4; version 4.5
Consensus quality: 219100 bases at least Q40
Consensus quality: 219278 bases at least Q30
Consensus quality: 219278 bases at least Q30
Consensus quality: 219278 bases at least Q30
Consensus quality: 219378 bases at least Q30
Consensus quality: 219378 bases; agarose-fp
Quality coverage: 8.13x in Q20 bases; sum-of-contigs Quality
coverage: 8.37x in Q20 bases; agarose-fp
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100.0%; Pred. No. 3.4e+02;
:ive 0; Mismatches 0;
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1. .50258
/note="assembly_fragment:00500"
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                                                                                   Center: Wellcome Trust Sanger Institute
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-22301"
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Best Local Similarity 100.0
Matches 19; Conservative
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                                                                                                                Center code: SC
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                                                                                                                                                                                   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations regether with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, SMISSERCY: T:: TREMBL; WP:, WORNPEP: Information on the WORNPEP database can be found at their wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of monouncleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submired.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). The further information see http://www.sanger.ac.uk/Projects/D rerio/fishmask.shtml CH211-208D15 is from a CHORI-211 BAC library
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Actinopterygii, Neopterygii; Teleostei, Ostariophysi,
Cyptiniformes, Cyprinidae, Danio.
1 (See 1 to 219601)
Phillimore,B.
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Submitted (04-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
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  BX649641.7 GI:38198314
HTG: HTGS PHASE1; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Danic rerio (zebrafish)
Danic rerio
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100.0%; Pred. No. 3.4e+02;
iive 0; Mismatches 0; Indels
                                                                                                                Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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/clone="CH211-208D15"
/clone_lib="CHORI-211"
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BX649641/c
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TITLE
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/trānslation="SGYVGTALSLLIRAELGOPGALLGDDQLYNVIVTAHAFVMIFFL
WYPPLASKLANGVELMISPLANGVESTIGAVNFITTIILSSAAVESGAGTGWT
VYPPLASKLAHAGGSVVELAIFSLHLAGVSSTIGAVNFITTIINKKWRMQFEKLPLFV
WSVKTTAILLLLSLEVLAGAVTMLLTDRNFNTAFFDPAGGGDPILY"
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Phylogenetic relationships within the aquatic snail genus Tryonia:
implications for biogeography of the North American Southwest
Mol. Phylogenet. Evol. 13 (2), 377-391 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       country="Australia:tributary of Thirteen Mile Creek"
                                                                                                                                                                     Direct Submission
Submitted (18-FEB-1999) Biology, Southwest Missouri State
University, 901 S. National Ave., Springfield, MO 65804, USA
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Helix Research Institute (JP) ; Research Association for
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|rrans] table=5
|producE=cytcohrome c oxidase subunit I"
|protein_id="%AD39432.1"
|db_xref="G1:5081539"
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Pred. No. 1.5e+03;
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Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                     /organism="Phrantela marginata"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/db_xref="taxon:93097"
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AX713938
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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90.9%;
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                                                                                                                                                       Liu, H. P.
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                                                                                                                                                                                                                                               During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm: KBLIS Sw: SWISSPROY; Tr: TREMBL: Wp: WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived length of monounciectide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-151P17 is from a Zebrafish BAC library VECTOR: pIndigoBAC-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 23, 2003 this sequence version replaced gi:33386634.
          (23-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
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Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Rissooldea; Hydrobiidae; Phrantela.
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                                                                                                             Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                               Web site: http://www.sanger.ac.ux
Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
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AF129331.1 GI:5081538
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KEYWORDS SOURCE ORGANISM

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DEFINITION ACCESSION

RESULT 8 AF129331

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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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                                                                                                                                                                             2 (bases 1 to 11447)
Ren,S., Fu,G., Jiang,X., Zeng,R., Xiong,H., Lu,L., Lu,G., Jiang,H.,
Ding,Y., Jia,J., Tu,Y., Gu,W., Cai,Z., Sheng,H., Yin,H., Zhang,Y.,
Zhu,G., Wang,S., Shen,Y., Qiang,B., Chen,Z., Wen,Y., Xu,J. and

    11447
    Organism="Leptospira interrogans serovar lai str. 56601"
/mol_type="genomic DNA"
/strain="56601"

Shen,Y., Qiang,B.Q., Xia,Q.C., Guo,X.K., Danchin,A., Saint Gixons,I., Somerville,R.L., Wen,Y.M., Shi,M.H., Chen,Z., Xu,J.G. and Zhao,G.P.
                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (12-MR-2002) Chinese National Human Genome Center at Submitted (12-MR-2002) Chines Road, Shanghai 201203, China Updated information will be available at our World Wide Neb site (http://www.chgc.sh.cn/lep/). Comments to the authors are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Strain 56601 is maintained by the Institute Bpidemiology and Microbiology, Chinese Academy of Preventive Medicine"
                                                                        Unique physiological and pathogenic features of Leptospira
interrogans revealed by Whole-genome sequencing
Nature 422 (6934), 888-893 (2003)
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protein id="AAN48518.1"
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144..701
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db_xref="taxon:189518"
chromosome="I"
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841. .91
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2674. _2814
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2 {bases | to 3727}

Stagair. Otsuki, T. and Sugiyama, T.

Direct Submission

1. Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,

Genomics Laboratory, 1332-3 Yana, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomicsGhri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of

Ronomy, Trade and Industry of Japan, CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA ilbrary

Construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Byaluation; clone selection for full insert sequencing: RAB and
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AE011312 AE010300
AE011312.1 GI:24194885
                                                                                                                                                                                                                                                                                                                                       Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Pukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                 PRI 01-AUG-2002
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Leptospira interrogans serovar lai etr. 56601
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
I (bases 1 to 11.447)
Ren, S.X., Fu, G., Jiang, X.G., Zeng, R., Miao, Y.G., Xu, H., Zhang, Y.X., Xiong, H., Lu, G., Pu, L.F., Jiang, H.Q., Jiang, T.Y., Liang, Y.Q., Cai, Z., Sheng, H.H., Yin, H.F., Zhang, Y.X., Zhang, Y.Q., Cai, Z., Sheng, H.H., Yin, H.F., Zhang, Y. Zhang, Y. Q., Cai, Z., Sheng, H.L., Qian, Z., Wang, S.Y., Ma, W., Yao, Z.J.,
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                            Homo sapiens cDNA FLJ31315 fis, clone LIVER1000303.
AK055877 AK055877 GI:16550712
Ak055877 GI:16550712
Homo sapiens (human)
File sapiens
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3 (bases 1 to 39574)
Bourbon, H.M.
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Drosophila melanogaster Toutatis (tou) gene, complete cds.
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Drosophila melanogaster

Bukarycta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukarycta; Budopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

[ Dases 1 to 39574)

Fauvarque, M.O., Laureni, P., Boivin, A., Bloyer, S., Griffin-Shea, R., Bourbon, H.M. and Dura, J.M.

Dominant modifiers of the polyhomeotic extra-sex-combs phenotype induced by marked P element insertional mutagenesis in Drosophila Genet. Res. 78 (2), 137-148 (2001)
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Submitted (18-OCT-2000) Centre de Biologie du Developpement,
CNRS/UPS, 118 Route de Narbonne, Toulouse, HG 31062, France
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37500. .38602)
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TREDPCVDVRQIFDNCEMFNEDDSPVGKAGHGMRKFPESRWGBLFDKHS*
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Direct Submission
Submitted (19-189-1999) Celera Genomics, 45 West Gude Drive,
Bockville, MD, USA
This sequence was identified as CDM:10212756 by the submitter
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
the accession number will be preserved.

Location/Qualifiers
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|db_xref="taxon:7227"
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81.7%; Score 18.8; DB 3;
Best Local Similarity 90.9%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 2;
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2 (bases 1 to 112659)
Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                               University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (Pases 1 to 112659)
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Nov 30, 2000 this sequence version replaced gi:7630788.
Submitted (17-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mn 6 3108, USA.
3 (Dases 1 to 112659)
                                                                                                     Direct Submission
Submitted (30-NOV-2000) Genome Sequencing Center, Washington
Notversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 112659)
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Submitted (17-58P-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 184, UK. B-mail enquiries.
Zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 18, 2003 this sequence version replaced gi:32398550.
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Gatinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 11959s)
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Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- Genome Center ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute Center: Center code: St. Www.sanger.ac.uk Web site: http://www.sanger.ac.uk Contact: zfish-help@sanger.ac.uk
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/mol_type="gencmic DNA"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission conty a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality: >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm., EMBL; Sw., SWISSEROT; Tr., TREMBL; Wp., WORMPEP; information on the WORWPEP database can be found at the both of subclones occasionally display inconsistency over the length of monouncleotied A/T runs and conserved TA repeats. Where
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-11N4 is from a Zebrafish BAC library
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nu	nucleic search, using sw model
Run on:	May 26, 2004, 15:20:44; Search time 292.115 Seconds (without alignments) 3115.905 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-676-299-8 21 1 taaccaaaacgcatatgatt 21
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 segs, 21671516995 residues
Total number of	hits satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: 0 length: 2000000000
Post-processing	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	X16045 E. coli R-f	AP005147 Salmonell	AC084483 Caenorhab	Z79756 Caenorhabdi	AF314193 Drosophil	AC020320 Drosophil	AC011696 Drosophil	AC007473 Drosophil	AE003825 Drosophil	AL049867 Human DNA	AC008057 Homo sapi	AC007630 Homo sapi
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ouerv	Match	100.0	100.0	87.6	87.6	87.6	87.6	87.6	87.6	87.6	85.7	85.7	85.7
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A7314193 Drosophil AC020320 Drosophil AC020320 Drosophil AC007473 Drosophil AL049867 Human DNA AC008057 Homo sapi AC06894 Buthus oc AJ506894 Buthus oc AJ506894 Buthus oc AJ506896 Buthus oc AJ506896 Buthus oc AJ506897 Buthus oc AJ506901 Buthus oc AJ50701 Mesobuthu AJ50701 Mesobuthu AJ50701 Mesobuthus AJ7394 Adforction AJ7383 Mouse DNA BK62944 Danio rer AP004317 Oryca sat AC11379 Rattus no AC11379 Rattus no AC113696 Rattus no AC113696 Rattus no AC116665 Rattus no AC116665 Rattus no AB024528 BX005451 0 AR274513 1 AP003688 110220 127887 110000

## ALIGNMENTS

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E. coli R-factor R773 arsR gene.
X16045
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Arshort resistance, arsR gene, ArsR protein; DNA-binding protein, regulatory protein; resistance gene.
Bscherichia coli
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1. (Dases 1 to 727)
San Francisco,M.J., Hope,C.L., Owolabi,J.B., Tisa,L.S. and Rosen,B.P. RESULT.1 BCRFARSR/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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Furuya, N. and Komano, T. Mutational analysis of the R64 oriT region: requirement for precise location of the NikA-binding sequence J. Bacteriol, 179 (23), 7291-7297 (1997)
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Purification and characterization of thin pili of IncIl plasmids
Purification and starterization of Pilv-specific cell aggregates by type IV pili
J. Bacteriol. 180 (11), 2842-2848 (1998)
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Surface exclusion gene of Incil plasmid R64: nucleotide sequence
and analysis of deletion mutants
Plasmid 32 (1), 80-84 (1994)
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gene for plasmid
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Requirement of a limited segment of the sog gene for plasmid R64
conjugation
Plasmid 38 (1), 1-11 (1997)
                                                                    Nisioka, T.
oriT region of the IncIl
                                                                                                                                                                                   Furuya,N., Nisioka,T. and Komano,T.
Nucleotide sequence and functions of the oriT operon in Incl1 plasmid R64
J. Bacteriol. 173 (7), 2231-2237 (1991)
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The plasmid R64 thin pilus identified as a type IV
J. Bacteriol. 179 (11), 3594-3603 (1997)
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Nucleotide sequence and characterization of
Incll plasmid R64
J. Bacteriol. 175 (16), 5035-5042 (1993)
                                                     Komano,T., Toyoshima,A., Morita,K. and Cloning and nucleotide sequence of the plasmid R64
                                                                                                             J. Bacteriol. 170 (9), 4385-4387 (1988)
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 Genet. 213 (1), 30-35 (1988)
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A82. .511
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DNA, complete sequence.
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                                                                                                    Sosen, B.P.
Direct Submission
Submitted (09-AUG-1989) Rosen B.P., Department of Biochemistry,
Submitted (09-AUG-1989) Rosen B.P., Department of Biochemistry,
Wayne State University, School of Medicine, 54- B Canfield Avenue,
Detroit MI 48201, U S A
Location/Qualifiers
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Identification of the metalloregulatory element of the plasmid-encoded arsenical resistance operon Nucleic Acids Res. 18 (3), 619-624 (1990) 90174986
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/note="unnamed protein product; ArsR
                                                                                                                                                                                                                                                                                                                                                                                                                 'note="transcriptional start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                  114. .118
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/note="got. -35 region"
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Salmonella typhimurium plasmid R64 i
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Rtkrrrgehstychkyaperyralkgolghaymlukkdpytgesqlidmens
Repytyckrytychkyaperchldalwyllapessbagthygmsyytrlaeeispko
Seghyi peleytycskliabequeeyylgyleeetymdrehgqlipryvwi tpagwqw
Igydwythetgolgkelreseetroglireegyberededisyshaarkrylcksqdalkkr
Rekaaaskranrlikklipvdociyemaeetylkrrlippbbayrcsddelir
                                                                                                                                                                                                                                                                                                            15 (bases 1 to 120826)

Komano, T., Sasaki, T., Tachibana, K., Furuya, N., Saito, Y., Suzuki, T.,

Sampei, G. and Mizobuchi, K.

Direct Submission

Office Commission

Submitted (O7-MAY-2002) Gen-ichi Sampei, The University of

Submitted (O7-MAY-2002) Applied Physics and Chemistry; Chofugaoka

1-5-1, Chofu, Tokyo 182-8585, Japan (E-mail:sampei@pc.uec.ac.jp,

Tel:81-424-43-5481, Pax:81-424-43-5501)

10.120826
                                                                                                                                                                                                     Sasaki, T., Tachibana, K., Furuya, N., Saito, Y.,
                                                       Komano, T., Yoshida, T., Narahara, K. and Furuya, N.
The transfer region of Incli plasmid R64: similarities between R64
The transfer region of Incli plasmid R64: similarities between R64
The and legionella icm/dot genes
MOI. Microbiol. 35 (6), 1348-1359 (2000)
20223621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //notes=R86 strain drd-11"
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protein of insertion sequence IS2]
location complement(4143, .4147) and location
complement (20047, .20051) are dupulicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="repy"
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                                                                                                                                                                                                         Sampei, G., Komano, T., Sasaki, T., Tachibana, K., Furuya, N., Sait
Suzuki, T. and Mizobudhi, K.
Organization and diversification of plasmid genomes: complete
nucleotide sequence of R64 genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB91567.1"
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Submitted (04-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dupulicated"
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Caenorhabditis briggsae cosmid G03E09, complete sequence.
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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Washington University Genome Sequencing Center. The C. briggsae Genome Sequencing Project Unpublished
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Department of Genetics, Washingto
St. Louis, MO 63110, USA
e-mail: jspieth@watson.wustl.edu
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Waterston, R.
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Direct Submission

Direct Submission

Direct Submission

Submitted (04-287-1996) Nematode Sequencing Project, Sanger

Direct Submission

Submitted (14-287-1996) Nematode Sequencing Project, Sanger

Institute, Minxton, Cambridge CB10 18A, England and Department of

Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:

jesssanger.ac.uk or rwatemantode.wustl.edu

Coding Sequences below are predicted from

conjuter analysis, using

predictions from Genefinder (P. Green, U. Mashington), and other

available information.

Current Sequence finishing criteria for the C. elegans genome

sequencing consortium are that all bases are either sequenced

unambiguously on both strands, or on a single strand with both a

dye primer and dye terminator reaction, from distinct subclones.

Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis

see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?

IMPORTANT: This sequence is NOT necessarily the entire insert of

the specified clone. It may be shorter because we arrange for a small

Overlapping sections once, or longer because we arrange for a small

It may be shorter because we only sequence overlapping sections

Once, or longer because we arrange for a small overlap between

neighbouring submissions.

The true right end of clone F53CII is at 110263 in
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The end of this sequence (34695, .34796) overlaps with the start of
sequence CEF55B12.
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The true left end of clone F55B12 is at 34695 in this sequence. The
start of this sequence (1, .100) overlaps with the end of sequence
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Caenorhabditis elegans
Caenorhabditis elegans
                                                                                                                                                                                                                                                                        Gaps
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis
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                     Location/Qualifiers
1. 21479
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                                                                                                                                                                                                                        Score 18.4; DB 3;
Pred. No. 4.6e+02;
0; Mismatches 1;
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The C.elegans Sequencing Consortium.
2 (bases 1 to 34796)
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    neighboring submissions
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PUBMED
REMARK
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
CEF53C11
                          PEATURES
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SOURCE

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jóin(1651. .1903,25307. .25489,25552. .25797,26308. .26795,
26857. .27479,27542. .28784,28847. .29119,29355. .29711,
30457. .34467,35337. .35854,36084. .37248,37313. .37434,
37500. .38602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /notes="putative subunit of a chromatin-remodeling complex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Endoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Enhydroidea; Drosophilidae; Drosophila.
1 (Bases 1 to 39574)
Eauvarque, M.O., Laurenti, P., Boivin, A., Bloyer, S., Griffin-Shea, R., Bourbon, H.M. and Dura, J.M.
Dominant modifiers of the polyhomeotic extra-sex-combs phenotype induced by marked P element insertional mutagenesis in Drosophila Genet. Res. 78 (2), 137-148 (2001)
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF314193 39574 bp DNA linear INV 11-APR-2003
Drosophila melanogaster Toutatis (tou) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jóin(25363, .25489,25552, .25797,26308, .26795,26857, .2727542, .28784,28847, .29119,29355, .29711,30457, .34467, 35337, .35854,36084, .37248,37313, .37434,37500, .37656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 39574)
Bourbon, H.M.
The novel trx-G gene toutatis encodes a Drosophila member of the WAL family of chromatin-associated proteins
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (18-OCT-2000) Centre de Biologie du Developpement,
CNRS/UPS, 118 Route de Narbonne, Toulouse, HG 31062, France
Location/Qualifiers
1. .39574
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                          Length 34796;
                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                             Score 18.4; DB 3;
Pred. No. 4.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                              221 AACCAAAACGCATATAATT 240
                                                                                                                                                                                                                                                                                                            2 AACCAAAAACGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF314193.1 GI:12642597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               map="48A3-6"
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'gene="tou"
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Bourbon, H. M.
                                                                                                                                                                                                   87.6%;
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                                                                                                                                                                                                                                                     Conservative
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RRDRDRESGGSAKRRSDNSKTPAMEHMOOOOMPLAGGDSHHHTHQOPPSLNSSHDESM NSLPAGSSEVSVGACGRLNGRRSTRSGPOLINNASALCSPAHSVVSATIYYDDOHTANNS VDGSSRFHAHLIPPSNNGTAALLEDVPGGANVMPGVYPVYTPVAAGNPSAGLINQAPV QPAMPPANVVAMSPRÄVTPTRTRTPTPTPAPTPPPPPPPLIMQASPTATALHVÄACO SPOCOMPAGUTTMPSRPATGVGTATNAMONSPPPTINTALQEAKRKLKGOEKKEKHATKKL MKELAVCKTLLGEMELHEDSNPPLLPVATKOPPTRKT IKTPMDLSTIKKLQDLSYT TREDPCVDVRQIFDNCEMFNEDDSPVGKAGHGMRKFFBSRWGELTDKHS"

ö Similarity 95.0%; Pred, No. 4.16+02; Pred; Conservative 0; Mismatches 1; Indels 6; 19; Query Match Best Local Matches

2 AACCAAAACGCATATGATT 21 a

13571 AACCCAAAACGCATATGATT 13552

AC020320 LOCUS ACCESSION VERSION KEYWORDS SOURCE ORGANISM AC020320/c RESULT 6

74881 bp DNA linear HTG 03-JAN-2000 , \*\*\* SEQUENCING IN PROGRESS \*\*\*. AC020320.1 G1:6664577 HTG2 HTG3 PHASB2. Drosophila melanogaster (fruit fly) Drosophila melanogaster Drosophila melanogaster, AC020320 AC020320:1 GI:6664577

COMMENT

ACO11696 170869 bp DNA linear INV 23-MAR-2001 Drosophila melanogaster, chromosome 2R, region 48A-48C, BAC clone BACR35F01, complete sequence. Gaps Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

1. (bases 1 to 7481) Direct Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, Mp. USA.

Rockville, Mp. USA.

Rockville, Mp. USA.

ROTE: This sequence was identified as CDM:10212756 by the submitter.

For more information on this record e-mail to fly@celera.com.

NOTE: This is a "working draft" sequence.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

I. 74881 o; Query Match
87.6%; Score 18.4; DB 2; Length 74881;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; /organism="Drosophila melanogaster" /mol\_type="genomic DNA" /db\_xref="taxon:7227" 37442 AACCCAAAACGCATATGATT 37423 2 AACCAAAAACGCATATGATT 21 Adams, M. and Venter, J.C. AC011696 AC011696.4 GI:13435224 ACCESSION VERSION KEYWORDS SOURCE ORGANISM source LOCUS
DEFINITION REFERENCE AUTHORS TITLE JOURNAL RESULT 7 AC011696 REPERENCE FRATURES COMMENT ORIGIN 셤 ò

Drosophila melanogaster (fruit fly)

Brosophila melanogaster

Bukaryota; Metazoda Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Medazoda, Arthropoda; Hexapoda; Insecta; Pterygota;

Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Bydroidea; Drosophilidae; Drosophila.

Bydroidea; Drosophilidae; Drosophila.

Calniker; S.B., Adams, M.D., Kronmiller; B., Tyler, D., Wan, K.H., Adams, M.D., Amanatides, P.G., Brandon, R.C., Rogers; Y., An, H., Baldwin, D., Amanatides, P.G., Brandon, R.C., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Parfan, D., Ferriers, S., Frise, R. Galle, R.F., Gargy, N.S., George, R. A., Gonzalez, M., Houck, J., Hostin, R.A., Flostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Phouanenavong, S., Pittman, G.S., Patel, S., Petelffer, B., Phouanenavong, S., Pittman, G.S., Patel, S., Petelffer, B., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Sequencing of Drosophila chromosome 2R, region 48A-48C Submitted (11-07T-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Mar 23, 2001 this sequence version replaced gi:6119492. Loades 1 Lu J. Oversy,
Clanker, S. B., Agbayani, A., Arcaina, T. T., Baxter, B., Blazej, R. G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C. M., Farfan, D. B., Galle, R., George, R. A., Harris, N. L.,
Klan, R., Hummasti, S. R., Karra, K., Kearney, L.,
Kim, B., Lee, B., Lewis S., Li, P., Lomotan, M. A., Mazda, P.,
Moshrefi, A. R., Moshrefi, M., Nixon, K., Pacleb, J. M., Park, S.,
Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
Svirskas, R.R., Wan, K. H., Weinburg, T., Zhang, R., Zieran, L. L. and (bases 1 to 170869) Direct Submission Rubin, G.M. TITLE JOURNAL REFERENCE AUTHORS

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us-10-676-299-8.rge

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ACCESSION
VERSION
                JOURNAL
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AE003825
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Sequence submitted by:

Berkeley Drosophila Genome Project

Iawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu

Location/Qualifiers

i. .170869

/organism="Drosophila melanogaster"
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BBACe3.6)"
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Drosophila melanogaster
Eukaryoter, Metazoa, Arthropoda, Haxapoda, Insecta, Pterygota;
Bukaryotera, Endopterygota; Diptera, Brachycera; Muscomorpha;
Reoptera, Endopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Ecliniker, S. B., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K.H.,
Celniker, S. B., Adams, M. D., Banzon, J., Beson, K.Y.,
Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S. M.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S. M.,
Carlson, K., Dorsett, V., Doup, L. B., Doyle, C., Dresnek, D., Farfan, D.,
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Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Dodson, T.C., Moy, M., Wurphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Fleiffer, B.,
Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, P.,
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Thousalled of Drosophila chromosome 2R, region 48A-48B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC007473 171831 bp DNA linear INV 28-FEB-2001 Drosophila melanogaster, chromosome 2R, region 48A-48B, BAC clone BACT38D12, complete sequence.
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[Lases 1 to 171831]

[Calliker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Hunston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Pacleb, J.M., Packiffer, B., Poon, L., Sequeira, A., Sethi, H., Shir, S., Sairsks, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.E., and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.6%; Score 18.4; DB 3; Length 170869; Best Local Similarity 95.0%; Pred. No. 3.2e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC007473.10 GI:13162476
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JOURNAL
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AUTHORS
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AUTHORS
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AC007473
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TITLE

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Submitted (05-MAY-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 28, 2001 this sequence version replaced gi:5670618. Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. Por further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.@ww.fruitfly.org/sequence/) or send email
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Drosophila melanogaster chromosome 2R, section 25 of 74 of the
                                                                                                                                                                                                                                                                                                                                                                           /map="48A-48B"
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95.0%; Pred. No. 3.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete sequence.
AE003825 AE002787 AE013599
AE003825.3 GI:21627432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AACCAAAAACGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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DEPINITION
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SOURCE
ORGANISM
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9260. .41878

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differs from SWP:POSS27 after DRPSSG; nonconsensus splice
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                repeat_region
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2 (Dases 1 to 261690)
3 Celniker, S.E., Adams, M.D., Kronmiller, B., Wan, K.H., Holt, R.A.,
BVAIR, C.A., Goccayre, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y.,
Bvans, C.A., Goccayre, J.D., Amanatides, P.G., Brandon, R.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dadson, F., Dorsett, V., Doup, L.E., Doyle, C., Tesnek, D., Farfan, D.,
Ferriera, S., Frise, E. Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Libegwam, C., Jallai, M., Kruse, D., Li, P., Matteis, B., Mosthrefi, A.,
McIntosh, T.C., Moy, W., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Feiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Suriskas, R., Tector, C., Tyler, D.,
Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M.
Sequencing of Drosophila melanogaster genome
Unpublished
J. Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochnik, S.E.,
Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W.,
Celniker, S.E., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., de
Grey, A.D., J., Harris, N.L., Russo, S., Searle, S.M.J., Smith, B.,
Shu, S., Smutniak, P., Whitfield, E.J., Ashburner, M., Gelbart, W.M.,
Hanntain, G.M., Mandley, S.E.
McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N.V., Mobarry, C., Morry, J. Moshrefia, M. Kount, S.M., Moy, M., Murphy, B., Murphy, D., Muzhy, D.M., Nelson, D.E., Nelson, R.S., Nelson, K.A., Nixon, K., Nusskern, D.R., Pelazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puti, V., Reese, M.G., Reinert, K., Remington, K., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Yiamos, I. Simpson, M., Stupski, M.P., Shen, H., Shie, B.C., Siden-Yiamos, I. Stapheton, M., Stroski, M.P., Sunki, T. Tector, C., Turner, R., Vener, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodager, Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Yeb, R.F., Zhon, M., Zhang, G., Zhao, Q., Zhao, Q., Zhao, G., Zhao, M., Zhang, G., Zhao, G., Zhao, M., Zhang, G., Zhao, G., Zhao, M., Rubin, C., M., S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.M., Rubin, G.M., and Venter, J.C.
The genome sequence of Drosophila melanogaster
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Submitted (23-JAN-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
On Jun 28, 2002 this sequence version replaced gi:10727634.

Location/Qualifiers
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Direct Submitted (06-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 261690)
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Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
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Submitted (14-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, Calo 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 7, 1999 this sequence version replaced gi:4837713.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequencing problems, such chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was continmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL; Sw.; SWISSPROT; Tr.; TREMBL; We.; WORMPEP; Information on the WORMPEP that source and atabases can be found a att.; Annum cannot well as the sequence.
                                                                                                                                   SGXPINILAQSNAAANSSILSFSSSLANI CSNSNDSNSTATSSSTTNTSGAPVDLVKSPP
PAGAGAGTAGGGKSGEDSGTPTVPRAVYCTRYSDRFSGSGESTSAKAGAGGUVQPGR
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TVPSGQDALAQLTATRICGPGGAVIPHQQLLLQRDVHHHHHMQNHLNRRHHERA
LKFSIDNILKADFGSRLPRIGALSGNIGGGSVSGSSTGSSKNSGNTNGNRSPLKAPKR
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http://www.sanger.ac.uk/HGP/Chr20
Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="CG17835"
/note="inv gene product from transcript CG17835-RC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSJ738I16 96444 bp DNA linear PRI 1
Human DNA sequence from clone RP4-738I16 on chromosome
20p11.22-12.2. Contains STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.4; DB 3; Length 261690;
Pred. No. 2.9e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                             join(10671, .11968,40764, .40924,41344, .41585)
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Best Local Similarity 95.0%;
Matches 19; Conservative 0
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Homo sapiens
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HSJ738116 RESULT 10

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COMMENT

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VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
R47-738116 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP4-738116 is at 96444 in this
sequence. The true right end of clone RP5-106901 is at 101 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  716. 5904
hote="LiMC5 repeat: matches 7338. 7526 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LiMB repeat: matches 5387, .5456 of consensus"
512. .4873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "note="Line repeat: matches 5733. .5791 of consensus"
[2172. .12213
[note="LiP5 repeat: matches 5617. .5657 of consensus"
[2244. .12334
[2244. .12334
[244. .123606]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 1221. .1435 of consensus" 1821. .11901 note="MIR repeat: matches 12. .97 of consensus" 1908. .11941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MERSB repeat: matches 1. .175 of consensus" 0017. .10149 incte="MERSA repeat: matches 10. .174 of consensus" 11276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="FLAM C repeat: matches 4. .133 of consensus"
1590. .11816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L2 repeat: matches 2061. .2219 of consensus" 3617. .13720
                                                                                                                                                                                                                                                                                                                                                            note="FLAM A repeat: matches 1. .132 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="THRIB repeat: matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MER83 repeat: matches 1. .448 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSg repeat: matches 1. .303 of consensus"
4413. .4478
                                                                                                                                                                                                                                                                                                                                                                                                     note="THR1B repeat: matches 3. .71 of consensus" 083. .3383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note=*MIR repeat: matches 53. .262 of consensus* 3110. .13258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 16. .209 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 21. .259 of consensus"
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/norte="match: STS: Em:AU025603 Em:AU047422"
complement(15204. .15238)
/norte="match: STS: Em:AU024963 Em:AU026718"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="LIMCS repeat: matches 7084. .7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="17 copies 2 mer ac 91% conserved" 2082. .12140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="LTR10D repeat: matches 1. .513 of 4648. .14728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="52 copies 2 mer tt 60% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                             note="match: GSS: Em:AQ245299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15204. .15240
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7006="L1MC4 repeat: matches 7098. .7838 of consensus"
191411. 19415
700ce="L2 repeat: matches 2405. .2705 of consensus"
19519. .19746
700ce="MIR repeat: matches 2. .236 of consensus"
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| hote="LiM4 repeat: matches 3177. .4628 of consensus"
19001. .29496
| hote="LiMB5 repeat: matches 5453. .5979 of consensus"
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6897. .17025
"note="L1MC4 repeat: matches 7855. .7977 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5898 of consensus"
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Thote="Link repeat: matches 2177. .3186 of consensus"

Thote="match: $720. .27091)

Thote="match: $75: Em:Li6406"

6831, .26965

Thote="Link repeat: matches 3292. .3447 of consensus"

77031. .27088
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22773. .23076
"note="AluY repeat: matches 1. .303 of consensus"
13673. .23832
"note="Lift repeat: matches -11. .147 of consensus"
13860. .23991
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:ote="MLT2CB repeat: matches 3. .453 of consensus"
7512. .28992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 17, .260 of consensus" 6353. .16716
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2372. .22411
note="20 copies 2 mer tg 80% conserved"
2526. .22609
                                                                                                                                                                                                                                                 Troce="match: STS: Em:AJ026333"
15204. .1523
Troce="match: STS: Em:AJ027699"
15472. .15643
Troce="LIMC4 repeat: matches 5730.
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note="AluSc repeat: matches 1.
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note="match: GSS: Em:AQ344412"
6488. 33879
                                                /note="match: STS: Em:AU047995"
complement(15204, 15236)
.15237)
     complement (15204.
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CE 2 (bases 1 to 119082)

RS McCombie, W.R.

Direct Submission

Submitted (17-U11-1999) Litta Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA

On Oct 11, 2000 this sequence version replaced gi:9954568.

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is of a contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* truns of N, but the exact sizes of the gaps are unknown.

* This record will be undated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Homo sapiens chromosome 20 clone P1-10263, WORKING DRAFT SEQUENCE,
3 unordered pieces.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 119082)
                           1 39004. .39135
| 700te="F9LAM C repeat: matches 1. .127 of consensus" 1 30005. .39175
| 700te="F9LAM C repeat: matches 2. .160 of consensus" 1 39294. .39381 | 700te="MERSA repeat: matches 53. .126 of consensus" 1 39466. .39824 | 700te="MERS3b repeat: matches 13. .384 of consensus" 1 39827. .39885 | 700te="MERS3b repeat: matches 13. .384 of consensus" 1 39827. .39885 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662. .42844 | 700te="MERS3b repeat: matches 133. .189 of consensus" 1 42662 | 700te="MERS3b repeat: matches 133. .1895 | 700te="MERS3b repeat: matches 133. .1895 | 700te="MERS3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 96444;
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68532 68631: gap of unknown length
68632 102563: contig of 33932 bp in length
102564 102263: gap of unknown length
102664 119082: contig of 16419 bp in length.
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Pred. No. 5.3e+02;
0; Mismatches 0; Indels
/note="L2 repeat: matches 2101.
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Human Genomic Sequence, Chromosome 20
Unpublished
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AC008057.4 GI.10765024
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOmo sapiens (human)
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/clone="P1-10263"
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ilarity 100.0%; Pr
Conservative 0;
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Submitted (12-May-1999) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA

S (bases 1 to 16949)

G la Bastide, M., Gmoji., Dedhia, N.N., Matero, A., Ning Huang, E.,
O'Shaugnessy, A., Preston, R., Rodriguez, M., Schutz, K., Shah, R.,
Shekher, M., Spiegel, L., Swaby, I., Vill, D. and McCombie, W.R.
Direct Submission

L Submitted (02-JJL-1999) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA

S (bases 1 to 169494)

Sis McCombie, W.Richard.

Direct Submission

Submitted (18-NOV-2000) Cold Spring Harbor Laboratory

C Thlo Transposon removed.

Shocombie, W. Richard.

Shocombie, W. Richard.

Shocombie, W. Richard.
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Buthus occitanus mardochei partial mitochondrial COI gene for cytochrome oxidase subunit I, haplotype AG4a.

AJ506884

AJ506884.1 GI:28865338

COI gene; cytochrome oxidase subunit I.
                                                                                                       AC007630 169494 bp DNA linear PRI 22-NOV-2000
Homo sapiens chromosome 20 clone P1-7739, complete sequence.
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On Nov 21, 2000 this sequence version replaced gi:5332384.
On lov 21, 2000 this sequence version replaced gi:5332384.
Chone Pl-7139 contains a 3 kb overlap with Clone 48F5. The overlap ends at base 2940. From position 154930-155350 the subclones were single stranded and had single chemistry.
Location/Qualifiers
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1 (bases 1 to 169494)
McCombie,W.R.
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Transposon, totalling 1328bp, was removed from final
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Matches 18; Conservative 0; Mismatches 0; Indels 0
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/mol_type="genomic DNA"
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85514 AACCAAAAACGCATATGA 85497
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HTG.
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Homo sapiens
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BOC506884/c
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Buthus occitanus mardochei partial mitochondrial COI gene for cytochrome oxidase subunit I, haplotype HAlb.
AJ506893
COI gene: Cutocher
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The phylogeographic importance of the Strait of Gibraltar as a gene flow barrier in terrestrial arthropods: a case study with the scorpion Buthus occitanus as model organism Mol. Phylogenet. Evol. 28 (1), 119-130 (2003)
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PRMNNMSFWLLPPAFFLLISSALLESGAGTGWTVYPPLSSSLAHMGGSVDLTIFSLHL
AGVSSILGAINPITTIINMSMGMTLDKVPLFVWSVFVTAVLLLLSLPVLAGA"
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mitochondrion Buthus occitanus mardochei (Moroccan scorpion)
Buthus occitanus mardochei
Bukaryota; Metazoa; Arthopoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.
mitochondrion Buthus occitanus mardochei (Moroccan scorpion)
Buthus occitanus mardochei
Bukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.
                                                                                                                Gantenbein, B. and Largiader, C.R.
The phylogeographic importance of the Strait of Gibraltar as a flow barrier in terrestrial arthropods: a case study with the scorpion Buthus occitanus as model organism Mol. Phylogenet. Evol. 28 (1), 119-130 (2003)
                                                                                                                                                                                                                                                                               2 [bases 1 to 466]
Gantenbein, B.
Direct Submission
Submitted (26-AUG-2002) Gantenbein B., ICAPB, University of
Edinburgh, West Mains Road, Edinburgh EH9 3JT, UNITED KINGDOM
Location/Qualifiers
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/organism="Buthus occitanus mardochei"
/organism="Buthus occitanus mardochei"
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/mol_type="genomic DNA"
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/sub species="mardochei"
/db xref="taxon:6869"
/haplotype="A64a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               country="Morocco:Immousser valley, Agadir region" 466
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84.8%; Score 17.8; DB 3; Length 466;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="COI"
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Gantenbein, B.
Direct Submission
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Query Match

84.8%; Score 17.8; DB 3; Length 466;

Best Local Similarity 90.5%; Pred. No. 1.7e+03;

Matches 19; Conservative 0; Mismatches 2; Indels
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                                              Buthus occitanus mardochei partial mitochondrial COI gene for cytochrome oxidase subunit I, haplotype HAZa.
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COI gene; cytochrome oxidase subunit I.
mitochondrion Buthus occitanus mardochei (Moroccan scorpion)
Buthus occitanus mardochei
Bukaryote; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/species="mardochei"
/specinen_voucher="A. Scholl, 15-II-1999 (NHMBE, CH)"
/db xref="Exaxoni6869"
/haplotype="HA2a"
/country="Morocco:Agouim, Haut Atlas"
/gene="COI"
/gene="COI"
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Submitted (26-AUG-2002) Gantenbein B., ICAPB, University of Edinburgh, West Mains Road, Edinburgh EH9 3JT, UNITED KINGDOM Location/Qualifiers
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The phylogeographic importance of the Strait of Gibraltar as a flow barrier in terrestrial arthropods: a case study with the scorpion Buthus occitanus as model organism books. Evol. 28 (1), 119-130 (2003)
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Submitted (25-A705-2002) Gantenbein B., ICAPB, University of
Edinburgh, West Mains Road, Edinburgh EH9 3JT, UNITED KINGDOM
Location/Qualifiers
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84.8%; Score 17.8; DB 3; Length 466;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels

    .466
    /organism="Buthus occitanus mardochei"

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Gantenbein, B.
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BOC506894/c
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VERSION
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Gaps

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Search completed: May 26, 2004, 17:22:24 Job time : 295.115 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	e e	BCARSRBC	AE000426	AE015361	AC145934	KCOOW 76	6861688	AE005575	BX545855	AP002565	AL954643	HS384F21	AL954640	AC084813	AX508952	AX346299	AB005234	AC002534	AL935136	AC145899	AC006459	AC119517	AC068945	BX546482	CNSOCKTE	103790	AC103972	AB046439	AC079617	AC103792	AC051625	AP003342	AC069557	AP003296	47005850	ACU 79055	AT.845504	AC126319	AC026402	AC138307	AC132596	AC068090 BX545912	34775	ALIGNMENTS			3492 bp	ab, ar		arsenace ressor; a		eria, Gammap Escherichia.	!	armor,J., Shinder,	
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arsenic detoxification and is conserved in gram-negative bacteria
J. Bacteriol. 177 (8), 2050-2056 (1995)
95238276
                                                                                                                                  J. (Lass)
Diorio, C.
Diorio, C.
Direct Submission
Submitted (06-JUL-1994) C. Diorio, McGill University, 3775
University Street, Montreal, Quebec, H3A 284, CANADA
Location/Qualifiers
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1 (Dases I to 1024).

1 (Dases I to 1024).

Rilet, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.P., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.

The complete genome sequence of Escherichia coli K-12

Science 277 (5331), 1453-1474 (1997)
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This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NGHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 (e-mail: mark@anber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG
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Submitted (16-JA-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Emall: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Blattner, F.R.
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Plunkett, G. III.
Direct Submission
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function="enzyme; Degradation of proteins, peptides,

Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli fttp://www.genetics.wisc.edu). \*\*\* The E. coli K12 sequence and its annotations are periodically updated, this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of alabels. This should allow them to be searched for in Entez as gene

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gene

SGO

/note="synonym: b3498" complement(2439. .4481) /gene="prlC"

gene

CDS

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/function="orf; Unknown"
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equal length to YHIR\_ECOLI SW: P37534"
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gene

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Shigella flexneri 2a str. 301
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.

1 (bases 1 to 11524)
Jin,O., Yana,Z.H., Xu,J.G., Wang,X., Shen,Y., Lu,M.C., Wang,J.H.,
Liu,H., Yang,J., Yang,F., Qu,D., Zhang,X.B., Zhang,J.Y., Yang,G.W.,
Wu,H.T., Dong,J., Sun,L.L., Xue,Y., Zhao,A.L., Gao,Y.S., Zhu,J.P.,
Kan,B., Chen,S.X., Yao,Z.J., He,B.K., Chen,R.S., Ma,D.L.,
Qiang,B.Q., Wen,Y.M., Hou,Y.D. and Yu,J.
Qiang,B.Q., Wen,Y.M., Hou,Y.D. and Yu,J.
Genome sequence of Shigella flexneri 2a: insights into
pathogenicity through comparison with genomes of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jin,Q., Shen,Y., Wang,J.H., Liu,H., Yang,J., Yang,P., Zhang,X.B., Zhang,J.Y. Yang,G.W., Wu,H.T., Dong,J., Sun,L.L., Xue,Y., Zhang,J.Y., Yang,G.W., Zhu,J.P., Chen,S.X., Yao,Z.J., Wang,Y., Liu,W.C., Qiang,B.C., Wen,Y.M. and Hou,Y.D. Direct Submission
Submitted (08-MAY-2001) Microbial Genome Center of Chinese Ministry China. Public Health, 100 YingXin Jie, XuanMu Qu, Beijing 100052, P.R. China
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Shigella flexmeri 2a str. 301 section 324 of 412 of the complete
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                                                                                                                                                                                                             Gaps
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                                                                                                                                                                Length 10240;
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                                                                                                                                                                                                           0; Indels
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Nucleic Acids Res. 30 (20), 4432-4441 (2002)
12384590
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Pred. No. 11;
                                                                                                                                                                                                           0; Mismatches
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67._.1419
                                                                                                                                                                                                                                                                            7757 TTAAGTCATAIAIGTTTTTGACTTA 7781
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1 Similarity 100.0%;
25; Conservative 0)
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                                                                                                                                                                   Query Match
Best Local Similarity
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AUTHORS
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JOURNAL
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complement (2332. .2727)
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Query Match 100.0%; Score 25; DB 1; Length 11524; Best Local Similarity 100.0%; Pred. No. 11; Matches 25; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence of Gallus gallus clone Unpublished
                                                                                                                                     2229 TTAAGTCATATATGTTTTTGACTTA 2253
                                                                                                          1 TTAAGTCATATATGTTTTTGACTTA 25
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AC145934.1 GI:33386884
HTG; HTGS PHASE1.
Gallus gallus (chicken)
Gallus gallus
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1276;
22558;
33848;
33448;
5366;
6501;
7599;
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6088...7050

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PINSTREGGGYNPEQPDLAQQQLQQINACHTWTTYTNADYSKVVQLVSLINNIETIS
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae;
Phasianinae, Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2. (Dates 1 to 179941)
Wilson, R.K.
Direct Submission
Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6: contig of 1176 bp in length
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8: gap of unknown length
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13596:
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15012. 16279

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LOCUS

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                                          .1112)
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This sequence was determined as part of the B. coli Genome Project Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award #G00301 from the NIH Human Genome Project. The entire sequence was independently determined from B. coli MG1655; overlaps and conflicts with other sequence determinations are annotated. The start of this entry overlaps the start of the entry ECOUM82 (10328) by 547 bp.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaces; Escherichia.

1 (2025419)
Sofia, H.J., Burland, V., Daniels, D.L., Plunkett, G. III and Blattner, F. R.
Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to Bl.5 minutes
Nucleic Acids Res. 22 (13), 2576-2586 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-MAR-1994) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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V00039
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132284 TTAAGTCATATATGTTTTTGACTTA 132260
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PROGRESS ***, 6 unordered pieces.
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HTG; HTGS PHASE1.
Pan troglodytes (chimpanzee)
Pan troglodytes
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Microbiol. 2:767 (1988)"
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complement (6695. 6723)
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complement (6618. .15331)

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Best Local Similarity 100.0%; Pred. No. 6.1;
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Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 242495) Wilson,R.K.
Direct Submission
Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 242495) Wilson, R. K.
Direct Submission
Submirted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
On Nov 4, 2003 this sequence version replaced gi:33387136. \* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. ------ Summary Statistics -----Sequencing vector: M15; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least Q40
Consensus quality: bases at least Q20 3036. .4616 /note="assembly\_name:Contig14" 4717. .6291 /note="assembly\_name:Contig18" 6392. .8254 \_\_name:Contig19" /note="assembly\_name:Contig19" 8355. .242495 /note="assembly\_name:Contig20" 1370. .2935 /note="assembly\_name:Contig13" .. .1269 'note="assembly\_name:Contig12" The sequence of Pan troglodytes clone Unpublished misc\_feature misc\_feature

ORIGIN

AC146183 242495 bp DNA linear HTG 04-NOV-2003 Pan troglodytes chromosome y clone CH251-548L16, \*\*\* SEQUENCING IN

RESULT 6
AC146183
LOCUS
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us-10-676-299-9.rge

gene

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Shigella flexneri 2a str. 2457T section 15 of 16 of the complete
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Shigella flexneri 2a str. 2457T
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.

[ bases 1 to 289816)
Bournier, G., Mayhew, G.F., Plunkett, G. III, Rose, D.J., Darling, A., Mau, B., Perna, N.T., Payre, S. M., Runyen-Janecky, L.J., Zhou, S., Complete Genome Sequence and Comparative Genome Sequence and Comparative Genome Sequence and Comparative Genomics of Shigella flexneri Serotype 2a Errain 2457T
Infect. Immun. 71 {5}, 2775-2786 {2003}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 209816)
2 (bases 1 to 209816)
Wei.j., Goldberg.M.B., Burland, V., Venkatesan, M.M., Deng, W.,
Wei.j., Goldberg.M.B., Plunkett, G. III, Rose, D.J., Darling, A.,
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Mau, B., Perna, N.T., Payne, S.M., Runyen-Janecky, i.J., Zhou, S.,
Schwartz, D.C. and Blattner, P.R.
Submirsion
Submission
Submirted (13-UNN-2002) Genetics Laboratory, University of
Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
                                                  Gaps
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AE016992.1 GI:30043426
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/note="residues 1 to 208 of 208 are 88.94 pct identical to
residues 12 to 219 of 219 from Escherichia coli K-12 :
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1335...2165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="enzyme; Biosynthesis of cofactors, carriers: Biotin^{\pi}
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complement (3293. .3919)
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complement(2215, .3189)
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160. .6439
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/gene="bisC"
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66047 TTAAGTCATATATGTTTTGACTTA 66023
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AE005575.1 GI:12518196
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JOURNAL
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KEYWORDS
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/function="enzyme; DNA - replication, repair,
function=modification
/note="residues 1 to 187 of 187 are 97.32 pct identical to
residues 1 to 187 of 187 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Iocus tag="%4185"
/note="residues 1 to 146 of 146 are 97.94 pct identical to
residues 1 to 146 of 146 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="S4187"
/function="putative enzyme; Not classified"
/note="residues 1 to 232 of 232 are 99.13 pct identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MIRBAQRSELPAILESITYGHPFIKANYWRDCIPLVRDAY
LANAQWWWREDGKLLGPVSINGSRFLAAMFVAPKAVRRGIGKALMQYVQQRYEHLML
EVYQKOQPAIDFYRAQGFHIVOCAWQDETQLPFWIMSWPVVQTL"
complement (6845. .7408)
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switvlkkkrenyrayfrhofdpvxvaamqeedverlvqdagiirhrgkiqaiignaray
lqyrqukgepfpdfvwsfvnhopqvtqattlsbiptstsasdalskalkkrgfkfvgtt
icvsfmqacglvndhvvgcccylgnkp"
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residues 1 to 739 of 739 from Escherichia coli K-12
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product="3-methyl-adenine DNA glycosylase I"
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                                                              /codon_start=1
/transl_table=11
/product="blotin sulfoxide reductase"
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/db_xref="G1:3003432"
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/produce="hypothetical protein"
/protein id="AAP19153.1"
/db_xref="GI:30043433"
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Pred. No. 5.8;
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100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 5.8
Matches 25; Conservative 0; Mismatches
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db_xref="GI:30043434"
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complement(6845, 7408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKYNGPELTLTAFEPPASS"
complement (6408, ,6848)
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complement (6408. ,6848)
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/gene="yhjY"
/locus_tag="S4187"
7566. .8264
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transl_table=
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trans table=
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Escherichia coli 0157:H7 ED1933

Bacterichia coli 0157:H7 ED1933

Bacterichia coli 0157:H7 ED1933

Bacterichia coli 0157:H7 ED1933

Bacteria Proteobacteria; Echerichia.

Enterobacteriaceae; Escherichia.

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Rose, D. J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Grobeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Genome sequence of enterobaemorrhagic Escherichia coli 0157:H7

In Nature 409 (6819), 529-533 (2001)
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/gene="gor"
/function="enzyme; Biosynthesis of cofactors, carriers:
Thioredoxin, glutaredoxin, glutathione"
/note="Residues 1 to 450 of 450 are 99.33 pct identical to
residues 1 to 450 of 450 from Escherichia coli K-12 Strain
MgG155: B3500*
/codon start=11
/transl_table=11
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/product = "glutathione oxidoreductase"
/db_xref="Gl1:12518197"
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DNA linear BCT 21-MAR-2001
genome, contig 3 of 3, section 194
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/mol type="genomic DNA"
/strain="EDL933"
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/db_xref="taxon:155864"
/noce="enterohemorrhagic"
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/gene="arsR"
/note="synonym: 24903"
2300. .2653
/gene="arsR"
      AB005575
Bscherichia coli 0157:H7 EDL933
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/note="synonym: Z4900"
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/db_xref="G1:12518203"
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VNTTYNLMDYGYGAPWPEFGWGAPYYTNAVSQVTPELVK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 199 of 199 are 99.49 pct identical to of 199 from Escherichia coli K-12 Strain
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NGSYCSVPEANVSLSRKQHQVLSCIANQMTTEDILEKLKISLKTFYCHKHNIMMILNL
KRINELVRHQHIDYLV"
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                                                                                                                                                                 translation="MSIDFTPGMINTYHGDIXNRTTDTDNVKTPDTPMPPCDNREEQQ
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Anotes—0-faland #140; Region of the EDL933 chromosome not

homologous to E. coli K-12 MG1655"

complement (7845. .8873)
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/codon start=1
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/gene="slp"
/function="membrane; Cell envelop: Outer membrane
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/function="putative transport; Transport of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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/product="orf, hypothetical protein"
/protein id="AAG58639.1"
/db_xref="GI:12518204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function="orf; Unknown function"
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                                                                                               /protein_id="AAG58637.1"
/db_xref="GI:12518202"
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complement(7845. .8873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="synonym: Z4908"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="synonym: 24909"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Residues 1 residues 1 to 199
                                    codon start=1
transl table=11
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/gene="yhiF"
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/gene="yhiF"
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L Similarity 92.0%;
23; Conservative C
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Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="arsenical pump membrane protein"
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/translation="MLLAGAIFVLTIVLVIWQPKGLGIGWSATLGAVLALVTGVWHPG
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AAVAALFANDGAALITPIVIAMALLAGFSKGTTLAFVWAAGFIATRASLFILTVSNLV
NIVSADFFGLGFREYASVWVPVDIAAIVATLVMLHLYPRKDIPQNYDMALLKSPARAI
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ROPMOTVIPSELGWYLVVYGARAGGITEYLSGVLUNULADNGLWAATLGTGFLTAFLSSI
ROMMCFVLVGALSIDGSTAGGVIKEAMVYANVIGCDLGPKITPIGSLATLIMLHVLSG
KOMTISWGYYPRTGIIMTLPVLFVVILAALALRISFTL"
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/note="Residues 1 to 249 of 371 are 89.95 pct identical to
residues 1 to 249 of 260 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mSnitiyhnpacgtsrntlemirnsgteptiihyletpptrded
VKLIADMGISVRALLRKNVEPYEELGLAEDKPTDDRLIDFMLQHPILINRPIVVTTLG
TRLCRPSEVVLEIIPDAQXGAPTKEDGEKVVDBAGKRLK"
                                                       /note="Residues 1 to 117 of 117 are 94.87 pct identical to residues 1 to 117 of 117 from Bacherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                           /trānslation="msfildiolfkiladrtrigivilissigelcycolctaldoso
PKISRHIALIRESGILLDRKQGKWVHYRLSPHIPSWAAKIIEQAWRCEQEKVQVIVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Residues 1 to 429 of 429 are 100.00 pct identical
to residues 8 to 436 of 436 from Escherichia coli K-12
Strain MG1655: B3502"
function="regulator; Protection responses: Drug/analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="transport; Protection responses: Drug/analog
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/gene="arsC"
/note="synonym: Z4905"
4009. .4434
/gene="arsC"
/function="enzyme; Protection responses: Drug/analog
                                                                                                                                                                                                                                   repressor of chromosomal
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/note="No significant matches"
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/protein_id="AAG58635.1"
/db_xref="G1:12518200"
                                                                                                                                                                                              /transl_table=11
/product="transcriptional
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/db_xref="G1:12518201"
                                                                                                                                                                                                                                                                                                         id="AAG58633.1"
                                                                                                                                                                                                                                                                                                                                             'db xref="GI:12518198"
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?707. .3996
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/transl_table=11
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/gene="Z4907"
5062. .6177
/gene="Z4907"
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/gene="Z4906"
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/gene="arsB"
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Ohnishi,M.,
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                                                                                                                                                                                                      Direct Submission
Submitted (31-JU-2003) Wellcome Trust Sanger Institute, Hinxton, Submitted (31-JU-2003) Wellcome Trust Sanger Institute, Hinxton, Zabridgeshire, CB10 1SA, UK. B-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clone-requestGeanger.ac.uk
On Aug 1, 2003 this sequence version replaced gi:32187728,
Center: Wellcome Trust Sanger Institute
Center code: SC
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Center project Information
Center project Information
Center project name: zc212N6
Assembly program: Xc3A94, version 4.5
Assembly program: Xc3A94, version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 205928 bases at least Q40
Consensus quality: 206326 bases at least Q30
Consensus quality: 206336 bases at least Q20
Insert size: 207491; sum-of-contigs
Insert size: 207691; sum-of-contigs
Insert size: 207692; sum-of-contigs
Quality coverage: 10.18x in Q20 bases; sum-of-contigs Quality
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             EXS45855.2 GI:33412513
HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULITOP.
Danio rerio (zebrafish)
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1. .33257
/note="assembly_fragment:00933
fragment_chain:1
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/db_xref="taxon:7955"
/clone="CH211-212N6"
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                                                                                                                                                                                                           TITLE
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ACCESSION
             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURES
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267888 bp DNA linear BCT 07-MAR-2001
AP002565 BA000007
AP002565.1 GI:13363693
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Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishli,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
Complete nucleotide sequence of the prophage VT2-Sakai carrying the
verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
derived from the Sakai outbreak
Genes Genet. Syst. 74 (5), 227-239 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (sites)
Yokoyama, K., Makino, K., Kubota, Y., Watanabe, M., Kimura, S.,
Yutsudo, C.H., Kurokawa, K., Ishii, K., Hattori, M., Abe, H., Iida, T.,
Yamamoto, K., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Sacherichia coli K-12 strain M31655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of enterohemorrhagic Escherichia coli 0157,HT and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tamaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                               87.2%; Score 21.8; DB 2; Length 207991; ilarity 92.0%; Pred. No. 1e+02; Conservative 0; Mismatches 2; Indels 0;
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/note="assembly_fragment:01206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190319 TTABATCATATATGTTTTGATTA 190295
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Escherichia coli 0157:H7
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PUBMED

COMMENT FEATURES

SOS

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ge in 265 aa (Conserved in B.coli K-12)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/ridence=not_experimenta1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HA I TVYRODAQKLRKATLDTLALYLACGI DPEKST I FVQSHVPEHAQLGWALNCY TYFG
ELSRWTQFFDXSARYAEN INAGLFDYPVLMAAD I LLYQTNLVPVGEDQKQHLELSRD I
ARGRNALYGDI FKVPEPF I PKSGARVWSLLEPTKKMSKSDDNRNNY I GLLEDPKSVVK
KI TRAVYDSDEPPVYKTYDVQNKAGYSNLLD I LSAVTGOS I PELEKOFBGKYTGHLKGE
VADAVSGML FELQERYHRPRNDEA PLQQVMKDGAEKASAHASRTLKAVYEA I GFVAKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         벙
                                                                                                                               /hote="N-terminal part (1-115 in 294 aa) is similar t

XHPO GCOLI gi|1789773 percent identity 97 in 115 aa,

C-terminal part (162-294 in 294 aa) is similar to

XHPP_ECOLI gi|2367217 percent identity 99 in 133 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to N-terminal part (1-110 in 261 aa)
XHFQ ECOLI gi|1789775 percent identity 98 in 110 aa
(Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (5619. .6623)
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/gene="BCs4227"
complement(6616..7374)
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4691. .5488
/gene="ECs4225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ECs4224"
3872, .4204
/gene="ECs4224"
                                                 3045, .3872
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                                                                                                                                                                                                                                                                                                                    /codon_start=1
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IFVSVGEVARAAGTPWI.TVLAFVIGGLIVIPOMCYVARIENTAYPEWGADYYVIKOAGS
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RKRDDYKPLWRTPAFGLMTPLAIASSLLILVASTFVWADFIFGLICAVIVIATGLBAXRF
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Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-wail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen.info.osaka-u.ac.jp/
Pax:81-6-6879-2047)
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98 in 347 aa (Conserved in E.coli K-12)"
5 (bases 1 to 267888)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
Hayashi,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               producE="putative amino acid/amine transport protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sub_strain="RIMD_0509952"
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151_.318
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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151, .318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome project.
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                                       REFERENCE
AUTHORS
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JOURNAL
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gene

SOS

8

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Best Local Similarity 91.7%; Pred. No. 3e+02; Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                               HS384F21/c
                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mis subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm.; EMBL; Sw.; SWISSEROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at the WORMPEP atabases can be found at the prince of the control of the clone being a VAC.

from a Male (CSTBL/64) mouse BAC Library VBCTOR: PTARBACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
Gn Jun 27, 2003 this sequence version replaced gi:32131025.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 10.
Center Wellcome Center
Center Wellcome Trust Sanger Institute
/gene="ECs4227"
/note="similar to GPH ECOLI gi|1789787 percent identity 99
in 252 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                               AL954643 71661 bp DNA linear ROD 27-JUN-2003 Mouse DNA sequence from clone RP24-142A19 on chromosome X, complete sequence.
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 71661;
                                                                                                      Score 21.8; DB 1; Length 267888; Pred. No. 95; 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                  163563 TTAAACCATATATGTTTTTGACTTA 163587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/db_xref="taxon:10090"
                                                                                                                                                                                                                     1 TTAAGTCATATATGTTTTTGACTTA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="X"
/clone="RP24-142A19"
/clone_lib="RPCI-24"
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1, .71661
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                                                                                                         ch 87.2%;
1 Similarity 92.0%;
23; Conservative
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KEYWORDS
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AL954643/c
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DEFINITION
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone amen. Note that the variation amnotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was fainished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality; as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by respirations were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: FMBL; Sw: SWISSFROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the WORMPEP database can be found at the wormpep This sequence the prompart of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at the play the promptor or the library RPCI-3 constructed by the group of Pieter de Jong. For further details see three dong. For further details see the Jong. For further details see the WETOR: PCTARC?

IMPORTANT: This sequence is not the entire insert of clone NPG-TARCIANT: This sequence is not the entire insert of clone RP3-384721 in may be shorter because we sequence overlapping sections only once, except for a shorter verialp.

The true right end of clone RP4-809F4 is at 105 in this segmence.
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                                                                                                                                                                                                                                                                                                                                                              PRI 05-JUN-2003
                                                                                                                                                                                                                                                                                                                   H8384F21 96879 bp DNA linear PRI 05-JUN-200 Human DNA sequence from clone RP3-184F21 on chromosome 1424 Contains probable G protein-coupled receptor, EST, STS, CA repeat, aronates sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoja, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk
n July 15, 1998 this sequence version replaced gi:2980810.
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    Indels
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/db_xref="RZPD:RPCIP704F21384"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                            1 TTAAGTCATATATGTTTTTGACTT
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AL022171.1 GI:3319684
HTG; repeat polymorphism.
Homo sapiens (human)
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90039 TTAAGTCATATATTTTAGAGTT 90016
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 note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 5515. .6164 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                    334. 8604

505. .1974. repeat: matches 3562. .4840 of consensus"

505. .1974. repeat: matches 5333. .5524 of consensus"

833. .14099

note="LIPA2 repeat: matches 900. .6146 of consensus"
                                                                                                                                                                                                                                                                                                      47. .6840
|ote="LIM4 repeat: matches 3050. .3576 of consensus<sup>|</sup>
                                                                                                                                                   consensus
                                                                                                                                                                   217. 3451
note="LTTX24 repeat: matches 256. .490 of consensus"
                                                                                                                                                                                                                                       197. .3987
Note="LTR37A repeat: matches 79. .169 of consensus"
                                                                                                                                                                                                     505. .3791
matte="LTRZ4 repeat: matches 10. .198 of consensus"
                                                                                                                                                                                                                                                                                    .175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 1154. .1352 of consensus" 7756. .20873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L2 repeat: matches 1767. .2136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               793 .15867

iote="L2 repeat: matches 2672. .2746 of consensus"

7092 .17229

iote="L2 repeat: matches 912. .2167 of consensus"

228. .17414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2710 of consensus"
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.00te="ulnBAZ repeat: matches 2...776 of consensus"

.00te="1.1495

.00te="llME1 repeat: matches 5515...6164 of consens
                                                                                                                                                                                                                                                                                                                                        344. .7122
note="AluSx repeat: matches 3. .280 of consensus"
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85. .18000
                                                                                  .291 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ote="MIR repeat: matches 67. .260 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7449. .17525.
10te="MIX repeat: matches 29. .106 of consensus"
532. .17565
10te="17 copies 2 mer gt 91% conserved"
1534. .17565
1534. .17565
1534. .17864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="12 repeat: matches 638. .760 of consensus"
3288. .18442
                                                                                                                                        158. .3215
note="LTR37B repeat: matches 376. .430 of
                                                                                                                                                                                                                                                                                                                                                                                       copies 4 mer aaag 75% conserved"
                                                                                               523. 1684
note="81_copies 2 mer tt 59% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                         copies 2 mer ga 69% conserved"
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note="LTR33 repeat: matches 40.
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note="L2 repeat: matches 1187.
2401. .22700
                                                                                  note="AluSg repeat: matches 1.
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omplement(18864. 19338)
note="match: GSS: Em:AQ707236"
0299. .20485
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1634. .21945
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                              /clone="RP3-384F21"
/clone lib="RPCI-3"
256. .542
chromosome="1"
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note= 29 cc
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1ote="73
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                                                                                                             'note="Tigger2 repeat: matches 2546. .2707 of consensus" Note="Tigger2 repeat: matches 326. .856 of consensus" Note="Tigger2 repeat: matches 326. .856 of consensus" Note="LiPAl6 repeat: matches 5089. .6157 of consensus"
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/note="LiPAL6 repeat: matches 3643. .5085 of consens
42704. .45055
/hote="LiM2 repeat: matches 574. .2979 of consensus"
45056. .45375
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/47207
/note="match: GSS: Em:AQ676168" 48122. .48176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="12 repeat: matches 2588, ,2710 of consensus" 4246. ,34319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="Aludo repeat: matches 3. .245 of consensus"
17926. .37970
'note="MADEL repeat: matches 2. .50 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="FAM repeat: matches 84. .183 of consensus"
              complement (25242. .25840)
/note="match: GSS: Em:AQ552352"
complement (25484. .26006)
/note="match: GSS: Em:AQ665403"
26767. .26914
/note="FAM repeat: matches 5. .175 of consensus"
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Pred. No. 2.88+02;
0; Mismatches 2; Indels 0;
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14247. .34318
Thote=18 copies 4 mer tgtg 83% conserved"
14330. .34427
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note="42 copies 2 mer tt 65% conserved"
8438. ,38602
Em: AQ417112°
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idarity 91.7%;
Conservative 0
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Matches 22; Conserv
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us-10-676-299-9.rge

LOCUS DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

RESULT 13 AL954640

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Mammalia butnerlai Filates; Catarrini; Hominidae; Homo.

In Dases I to 151950)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sepiens chromosome 8, clone RP11-21H16

Enterpolation of the control of the con
naugedis
Homo sapiens chromosome 8 clone RP11-21H16 map 8, WORKING DRAFT
SACHSHOES, 28 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: 110793
Center clone name: 21 H 16
Center clone name: 21 H 16
Center clone name: 21 H 16
Center project name: 21 H 16
Center project name: 21 H 16
Center project name: 21 H 16
Center clone name: 21 H 16
Center clone name: 21 H 16
Consensus quality: 17649 bases at least Q40
Consensus quality: 17649 bases at least Q20
Consensus quality: 14462B bases at least Q20
Consensus quality: 14462B bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 176000; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-contigs
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247: gap of 100 bp
1339: contig of 1092 bp in length
                                                                                                                                                                                                 AC084813.1 GI:11225414
HTG; HTGS PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
HOMO sapiens
                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
    AC084813
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This sequence was fainished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL: Swi: SWISSPROT; TT:, TREMBL: WP:, WORMPEP; Information of the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JAN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, GB10 159, UK. B-mail enquirises:
Cambridgeshire, GB10 159, UK. B-mail enquirises:
On Jan 24, 2003 this sequence version replaced gi:27817477.
Sequence from the Mouse Genome Sequencing Consortium Whole genome Shotgum may have been used to confirm this sequence. Sequence abhorgum may have been used to confirm this sequence. Sequence are from the Whole genome shotgum alone has only been used where it has a phred quality of at least 30.
Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                    AL954640 112484 bp DNA linear ROD 24-JAN-2003 Mouse DNA sequence from clone RP23-65C22 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-65C22 is
from the RPCI-23 Mouse BAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3 6.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Mammalia; Butheria; Rodentia;
1 (bases 1 to 112484)
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                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
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AL954640.6 GI:27899738
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Direct Submission
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91478: contig of 14967 bp in length 479 91578: gap of 100 bp 756 102955: contig of 1177 bp in length 756 102855: gap of 100 bp 856 117027: contig of 14172 bp in length 128 130830: contig of 18703 bp in length 831 130830: contig of 18703 bp in length 131 151950: contig of 21020 bp in length 151950: contig of 21020 bp in length 15080: contig of 21020 bp in length.
Seconting of 1025 by in length of 100 by in le
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of 10412 bp in length
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of 14967 bp in length
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/mol_type="genomic DNA"
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Arabidopsis thaliana
Brastyca, Viridiplantaes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids II; Brassicales; Brassicaceae; Arabidopsis.
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83.2%; Score 20.8; DB 2;
Best Local Similarity 91.7%; Pred. No. 2.5e+02;
Matches 22; Conservative 0; Mismatches 2;
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Sequence 3647 from Patent W00216655.
AX508952
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Patent: WO 0216655-A 1647 28-FBB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
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                                                       Location/Qualifiers
1. .2000
7. Organism="Arabidopsis thaliana" /mol type="unassigned DNA" /db_xref="taxon:3702"
                                                                                                                                                                                                                            source
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Search completed: May 26, 2004, 17:22:30 Job time : 353.756 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic	search, using sw model
Run on: May	26, 2004, 15:20:44; Search time 347.756 Seconds (without alignments) 3115.905 Million cell updates/sec
Title: US-1 Perfect score: 25 Sequence: 1 ta	US-10-676-299-10 <sup>.</sup> 25 1 taagtcaaaaacatatatgacttaa 25
Scoring table: IDENT: Gapop	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched: 3470	3470272 seqs, 21671516995 residues
Total number of hits	s satisfying chosen parameters: 6940544
Minimum DB seq length: Maximum DB seq length:	th: 0 th: 2000000000
Post-processing: Mir Max Lis	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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: T3	em_htgo_other:*

Fig. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		coli gene Escherich	igella	llus ga	n trogl	Shigella	Escherich Danio rer	て.	Mouse DNA Human DNA	0 Mouse DNA	mo sapi	quence	abidops	abidops	Pan trogl	mo sapi	ttus no mo sapi	nio rer	Rattus no	a ent or mo sabi	mo sapi	Arabidops Homo gani	mo sapi	nomic S	Oryza sat	Genomic s Oryza sat	m	Homo sapi	ň	Mus muscu	n		nto sabi	Danio rer			-JUL-1995		camp;	•		) 1	functional in
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Escherichia coli K12 MG1655 section 316 of 400 of the complete
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1 (bases 1 to 10240)

Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Maynew, G.F., Mau, B. and Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-0CT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently denome Project and NCHGR). The entire sequence was independently frames were determined is coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, Kndly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG
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Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
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Submitted (02-SRP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Plunkett, G. III.
Direct Submission
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J. Bacteriol. 177 (8), 2050-2056 (1995)
95238276
                                                                                                                                         2 (fases 1 to 3492)
Diorio, C.
Diorio, C.
Submitssion
Submitted (Go.Jul-1994) C. Diorio, McGill University, 3775
University Street, Montreal, Quebec, H3A 2B4, CANADA
Location/Qualifiers
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Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, Kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edw). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version MS4. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein hinding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
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80

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Thioredoxin, glutaredoxin, glutathions"
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                                                                                                                       /note="f680; 100 pct identical to OPDA_ECOLI SW: P27298;
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/rzansl table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="yhiR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="factor Sigma70; predicted +1 start at 3640904"
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/note="factor Sigma70; predicted +1 start at 3642925"
1684. .5526
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Shigella flexneri 2a str. 301
Bacteria, Protebacteria, Gammaproteobacteria, Enterobacteriales,
Bacteria, Protebacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae; Shigella.

1 (bases 1 to 11524)
10, Wu. W. U. Wang, Y., Shen, Y., Lu, W. C., Wang, J. H.,
Liu, H., Yang, J., Yang, F., Qu, D., Zhang, X.B., Zhang, J.Y.,
Wu, H. T., Dong, J., Yang, F., Qu, D., Zhang, X.B., Gao, Y.S., Zhu, J.P.,
Kar, B., Chen, S., Yang, Z.J., He, B. K., Chen, R.S., Ma, D.L.,
Gang, B.Q., Wen, Y.M., Hou, Y.D. and Yu, J.
Genome sequence of Shigella flexneri 2a: insights into
pathogenicity through comparison with genomes of Escherichia coli
X12 and O157
Nucleic Acids Res. 30 (20), 4432-4441 (2002)
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Jin, Q., Shen, Y., Wang, J.H., Liu, H., Yang, J., Yang, F., Zhang, X.B.,
Zhang, J.Y., Yang, G.W., Wu, H.T., Dong, J., Sun, L.L., Xue, Y.,
Zhao, A.L., Qao, Y.S., Zhu, J.P., Chen, S.X., Yao, Z.J., Wang, Y.,
Lu, W.C., Qiang, B.O., Wen, Y.M. and Hou, Y.D.
Direct Submission
Submitted (108-MAY-2001) Microbial Genome Center of Chinese Ministry of Public Health, 100 YingXin Jie, XuanWu Qu, Beijing 100052, P.R.
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Shigella flexneri 2a str. 301 section 324 of 412 of the complete
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67. .1419
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AE015361.1 GI:24053992
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Best Local Similarity 10v..
These 25; Conservative
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AE015361/c
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ALHYSRWGNGRLLFTWIVLGAAVAALFANDGAALILFPIVIAMLALGESKGTTL
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LADNGLWAATLGTGFLFAFLSSIMNNMPTVLVGALSIDGSTASGVIKEAMVYANUGC
FALPALPERVAVVGAGYIAVELAGVINGLGAKTHLFVRKHAPLRSFDPMISETLVBVM NAGGEQLHTVAI PKAVVKNADGSLTILELEDGRSBTVDGLIATG GREABADNINLEAAG VKTNEKGYIVVDKYQWYNIELGIYAVGDYTGAVELTPVAVAAGRELSERLFNNKEDBHLD DYSNI PTVVPSHPPIGTOTVGLTEPPQARGYGODCYWCYKSSFTAMYTAVTTHROPCRMK LVCVGPEEKIVGIKGIGFGPGARGYGDAKAVAKKKSSFTAMYTAVTTHROPCRMK LVCVGPEEKIVGIKGIGFGMDEMLQGFAVALKMGATKKDFDNTVAIHPTAAEEFVTHR
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                                                                                                                                                                                                                                                                                                                                                                   131 are 100 pct identical to
aa protein from Shigella
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residues 37 to 167 of a 167
flexneri pir: T44475"
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                                                                                                                                                                                                                                               /locus_tag="SF3532"
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Wilson, R.K.
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WPLYESRLKGKLHVISKRYTQRIBRHNLANLRQHLARLVRKSLSFSKSVELHDKVIGHY
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AC145934 179941 bp DNA linear HTG 01-AUG-2003 Gallus gallus chromosome UNK clone CH261-4211, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 179941)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as 'runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                  Length 11524;
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                    DB 1;
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of 1268 b
unknown l
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100.0%; Pred. No. 11;
ive 0; Mismatches
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                                                                                                 Genome Center
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Wilson, R.K.
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Length 179941;
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Gaps

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TITLE

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TQQIQQKGWLNQQIKTQTQLQQQHLBNQINNNSQRYLQSQPGERNPARQQMLPNTNGG
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COMplement(1565. .2383)
/note="corresponds to_X14437; ECUGPQ(1. .819)"
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fivmygpsgcgkstllrmyaglervtegdimindorvtemepkdrgiamyfonyalyp
hmsvbenmamglkirgmgkoqiaervkeaarilbildgllkrrprelsgcgrgrvamgr
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WYNGGVABOTGTYVEVYERPSLEYRAS
INGGYRQYAGRRATGIRPERIALSSQAEGGVPMYMDTLEILGADNLAHGRWGEGKLV
VRLAHQBRPTAGSTLMLHLAENQLHLFDGSTGQRV"
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/note="CG Site No. 17794"
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/note="CG Site No. 17791; membrane protein"
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/product=21/ycerophosphocholine phosphodiesterase"
/proein_id=14Ab18424.1"
/db_xref="GI:466585"
                                                                                                                                                                        complement (1181, .2402)
'note="Corresponds to X56908; ECUGPQ2(1, .1222)"
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/note="corresponds to X13141; BCUGP(1. .4717)"
complement (2372. .3481)
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/note="predicted bend of 73.99 degrees"
                                                                                                                                                                                                                                                          .205. .1645
'note="alternate gene name yhhA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1693. .1727
/note="terminator-like sequence"
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'protein_id="AAB18425.1"
'db_xref="G1:912455"
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                                   complement (1085.
                                                                                                     complement (1146.
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                                                                                                                                                                                complement (1181.
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/codon_start=1
/transl_table=1
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                                                                              note="43%"
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Rakogawasvopatatovydvilkeggravdoskkslirhlaggtpgtygggsplir
Sknoyttavopatklardopivndoskkslirhlaggtpgtyrafgellld
Spilvopallaksleriardopivnoppykyvytlagdlayvykytphilkedlayvkvyry
Pisgdyrgyovysmpppssggihlivollilenpomkkygfgsdadamotnakaray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was determined as part of the E. coli Genome Project Frederick R. Blattner, director? at the University of Wisconsin-Madison. Supported by award #GG0301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps and conflicts with other sequence determinations are annotated. The start of this entry everlaps the start of the entry ECOUM92 (L10328) by 547 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Bscherichia.
I (asses I to 225419)
Sofia, H.J., Burland, V., Daniels, D.L., Plunkett, G. III and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-MAR-1994) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes
Nucleic Acids Res. 22 (13), 2576-2586 (1994)
                                                                                                                                                                                225419 bp DNA linear Bor region from 76.0 to 81.5 minutes.
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1067. .1094
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/note="CG Site No. 18280; cold-regulated"
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/protein_id="AAB18422.1"
/db_xref="G1:466583"
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132260 TAAGTCAAAACATATATGACTTAA 132284
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/strain="K-12"
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/db_xref="taxon:562"
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/transl_table=1
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E. coli chromosomal
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3036. .4616 // note="assembly_name:Contig14" 4717. .6291
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/note="assembly_name:Contig13"
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/note="assembly_name:Contig18"
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/note="assembly_name:Contig12"
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8355. .242495
/note="assembly_name:Contig20"
                                                                                                                                                                                                                                                                                  The sequence of Pan troglodytes clone
Unpublished
PROGRESS ***, 6 unordered pieces.
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/clone="CH251-548L16"
                                                                                HTG; HTGS PHASE1.
Pan troglodytes (chimpanzee)
Pan troglodytes
                                                             AC146183.2 GI:38154191
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GSRFYQTLALLPYAVAPAVAAVLMIFLFNPGRGLITHFLAEFGYDWNHAQNSGQAMFL
VVRSVWRQISYNELFPYAALQSIPRSLIEAAAIDGAGPIRRFFKIALDLIAPVSFFL
IVVNLVYAFFPTFPVITPATSGGPVQATTTLIYKIYREGFTGLDLASSAAQSVVLMFL
COMPLEMENT (5271. .6587)
                                                                                                                                                                                                                                                                  'Àb xref="GI:466588"
'translation="MSSSRPVFRSRWLPYLLVAPQLIITVIFFIWPAGBALMYSLQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pan troglodytes chromosome y clone CH251-548L16, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5826. .6859
Standard_name="REP; repetitive extragenic palindromic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="mRNh start determined by S1 mapping; Molecular Microbiol. 2:767 (1988)"
/evidence=experimental
complement(6651. .6679)
/note="inoludes pho box"
complement(6695. .6723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                 function="sn-Glycerol-3-phosphate transport system"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="sn-Glycerol-3-phosphate transport system"
/note="CG Site No. 39; periplasmic binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (6618, .15331)
/note="corresponds to J05516; ECOLIVHMGF(1, .8703)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 1; Length 225419; 100.0%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6836. .6837
/note="CG in J05516; GC in X13141 and here"
6845. .6846 ./note="C in J05516; CC in X13141 and here"
complement (6986. .7711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="T in X13141; G here"
6021. .6024
/note="GGCG in X13141; SSGS here"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                element"
/note="contains 1 RBP sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5473. .5474
/note="GC in X13141; SS here"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAB18428.1"
/db_xref="G1:466589"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TAAGTCAAAAACATATATGACTTAA 25
                                                                                                                                                                                                                                        id="AAB18427.1"
complement (4286. .5173)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (5271. .6587)
                                                             complement (4286, .5173)
                                                                                                                                              'note="CG Site No. 40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       table=11
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Matches 25; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="ugpB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="ugpB"
                                                                                             "ugpa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "76%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'trans]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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AC146183/c
LOCUS
DEFINITION
      gene
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Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 242495)
                                                                                                                                                                       Wilson,R.K.
Direct Submission
Direct Submission
Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 242495)
                                                                                                                                                                                                                                                                                                                                                       Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Nov 4, 2003 this sequence version replaced gi:33387136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of rea
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least Q40
Consensus quality: bases at least Q20
Consensus quality: bases at least Q20
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/locus tag="S4181"
/note="residues 1 to 276 of 276 are 94.56 pct identical to
residues 1 to 276 of 276 from Escherichia coli K-12 :
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/product="hypothetical protein"
/protein id="haPto]149.1"
/db xref="d1:30043429"
/translation="MILPGRLRRKGILQACPGLSLSRQTRVCRCALFLGERSKKWATG
rscsrkFAPLAALLMYVSLSGCFDKEGTORRAFTDFLQMYWRGSBERLFTLTADQKKQ
PGPFVSDYALLYGYSGQVNQAMDSGLRPVWDSVNALRYPQDYYTQSSPLREWMGSSLGV
IAAQQCQNAKLQADARBGALKQSDDLKRVFDQARTKVYTTPADALQPLIPAAQTFTQQL
/WYGDYIAQQGTQVSFVANGIQFPTSQQASBYNKLIAAPLPAQHQAFTQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus tag="S4182"
/function="putative enzyme; Not classified"
/note="residues 1 to 324 of 324 are 94.13 pct identical to
residues 5 to 328 of 328 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /traislation="MKPSVIINTALPDDLLQRLQAHPTVHQVANLSPQTVVQNAAIFA
EAEGLLGSNENVDAALLEKWPKLRATSTISVGYDNFDVDALTARKILLAHTPTVLTST
PADTLMALLACSARRVVEREVKAGERTASKIGDNYGTDVHHRTLGIVGMGIIGMAL
AQRVHPGFWNPILVRARRHEKRAEERFNARVCDLDTLLQESDFVGIILPLTDETTHLF
GAEQPAKMKSSAIFINAGRGPVVDENALIAALQKGEIHAAGLDVFEQEPLSVDSPLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /iocus tag="S4183"
/fuction="putative membrane, Not classified"
/note="residues 1 to 208 of 208 are 88.94 pct identical to
residues 12 to 219 of 219 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /t.ānslation="mggalavsgcttnpytgereagksalgaglygaglgalsss
Korgekgaligaaagalgcycytyhvygaalebkmggysytrschnillmpnn
Wfpsssallkraaamtlgvaavlkeypktavnvigytdstgchdlimplik
Vasalitggvdasrirtgglgpanplasnstabgkaonryeitlespl
                                                                         translation="MEYKDPMHELLSSLEQIVFKDETQKITLTHRTTSCTRIEQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="residues 21 to 759 of 759 are 98.78 pct identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tocus tag="84184" function="enzyme; Biosynthesis of cofactors, carriers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MANVVAVPHIGSATHETRYGMAACAVDNLIDALOGKVEKNCVNPHVAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transi_table=11
/producE="putative outer membrane protein"
/protein_id="AAP19151.1"
/db_xref="GI:30043431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
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/protein_id="AAR19150.1"
/db_xref="G1:30043430"
/product="hypothetical protein"
/protein_id="AAP19148.1"
/db_xref="G1:30043428"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="yiaB"
/locus_tag="S4182"
complement(2215. .3189)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="84183"
complement(3293. .3919)
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                                                                                                                                                   /locus_tag="S4181"
1335. .2165
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4160. .6439
                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=
                                                                                                        .335. .2165
'gene="yiaF"
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/gene="bisc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="yiaD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="yiaD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shigella flexneri 2a str. 2457T
Shigella flexneri 2a str. 2457T
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
Enterobacteriaceae; Shigella.
E (bases 1 to 289816)
S Wei J. Goldberg, W. B., Burland, V., Venkatesan, M. M., Deng, W., Fournier, G., Mayhew, G.F., Flunkett, G. III, Rose, D.J., Darling, A., Bau, J. Payne, S.M., Runyen-Janecky, L.J., Zhou, S., Schwartz, D.C. and Blattner, F.R.
Complete Genome Sequence and Comparative Genomics of Shigella flexneri Serotype 2a Strain 2457T
L Infect: Immun. 71 (5), 2775-2786 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus tag="S4180"
/note="residues 1 to 41 of 41 are 100.00 pct identical to
/note="residues 1 to 41 of 96 from Escherichia coli K-12 : B3555"
/codon start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                             AE016992 289816 bp DNA linear BCT 22-APR-2003
Shigella flexneri 2a str. 2457T section 15 of 16 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSGKMTGIVKWFNADKGFGFITPDDGSKDVFVHFSAIQNDGYKS
LDEGQKVSFTIESGAKGPAAGNVTSL"
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="regulator; Adaptations, atypical conditions" /note="residues 1 to 70 of 70 are 100.00 pct identical to residues 1 to 70 of 70 from Escherichia coli K-12 : B3556"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 289816)
Wei,J., Goldberg,M.B., Burland,V., Venkatesan,M.M., Deng,W.,
Wei,J., Goldberg,M.B., Burland,V., Venkatesan,M.M., Deng,W.,
Wourhier,G., Mayhew,G.F., Plunkett,G. III, Rose,D.J., Darling,A.,
Mau,B., Perna,N.T., Payne,S.M., Runyen-Janecky,L.J., Zhou,S.,
Schwartz,D.C. and Blattner,P.R.
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/product="cold shock protein 7.4, transcriptional
activator of hns"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-JUN-2002) Genetics Laboratory, University Wisconsin - Madison, 445 Henry Mall, Madison, MI 53706, Location/Qualifiers
1. .289816
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                           Length 242495;
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/mol_type="genomic DNA"
/strain="2457T"
                                                                               Indels
                                                                               ö
                              DB 2;
                           100.0%; Score 25; DB
100.0%; Pred. No. 6;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAP19147.1"
/db_xref="G1:30043427"
                                                                                                                                                              3353 TAAGTCAAAAACATATATGACTTAA 3329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'serotype="2a"
'db_xref="taxon:198215"
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complement(896. .1021)
                                                                                                                                1 TAAGTCAAAACATATATGACTTAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locus_tag="S4179"
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transl_table=:
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                                                                               25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       AE016992 AE014073
AE016992.1 GI:30
                                                      Similarity
                              Query Match
Best Local S
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AE016992
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TITLE

66023 TAAGTCAAAACATATATGACTTAA 66047

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FALPALPERVAVVGAGYIYNTBAGYNGETITANFHONGREPERPRODIINLEAMG
FALPALPERVAVCONTUNGELYAVELAGYNGARTHEVRENDELKSPDENISETLVEVN
NAEGPQLHTWAIPKAVVCNADGSLTLELEGGRSETVDCLIKAIGREPANDNINLEAMG
VKTNREKGYIVUDGGAYVTAGGAYTHAGOPCHKK
DYSNIPTUVPSHPPIGTUGLTEPQAREQYGDDQVKYKSSFTAMYTHAGPCRMK
XVCVGPEEKIVGIHGIGFGMDEMLQGRAVALKMGATKKDPDNTVALHPTAABEFVTMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sscherichia coli 0157:H7 EDL933

Sscherichia coli 0157:H7 EDL933

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

1 (bases 1 to 11071)

Perna, N.T., Pluukett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Svans, P.S., Gregor, J., Kirkpatrick, H.A., Posfâi, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apadca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R., in, J., Yen, G., Schwartz, D.C., Genome sequence of encerobaemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="gor"
/function="enzyme; Biosynthesis of cofactors, carriers:
Thioredoxin, glutaredoxin, glutathione"
Thote="Residues 1 to 450 of 450 are 99.33 pct identical to
residues 1 to 450 of 450 from Escherichia coli K-12 Strain
MG1655: B3500"
                                                                                                                                                                                                                                                              AE005575 11-MAR-2001
Escherichia coli 0157:H7 EDL933 genome, contig 3 of 3, section 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Perna, N.T., Plunkett, G., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anautharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Pelck, S. And Blattner, P.R.
Direct Submission
Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 45 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
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2300. ,2653
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AE005575 AE005174
AE005575.1 GI:12518196
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AUTHORS
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JOURNAL
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PUBMED
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
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/brotein id="AAP191"
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/db_xref="dl:30043453"
/db_xref=
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/function="enzyme; DNA - replication, repair,
restriction/modification"
/nore="residues 1 to 187 of 187 are 97.32 pct identical to
residues 1 to 187 of 187 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus tag="84185" / locus tag="84185" / note="residues 1 to 146 of 146 are 97.94 pct identical to residues 1 to 146 of 146 from Bscherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MERCGWVSQGPLYIAYHDNEWGVPETDSKKLFEMICFEGQAGL
SWITVLKKRENYRAYFHQFDPVKVAANQBEDYERLVQDAGIIHHGKLQAIIGNARAY
LQMEQNGEPFPDFVWSFVNHQPQVTQATTLSEIPTSTSASDALSKALKKRGFKFVGTT
ICYSFMQACGLVNDHVVGCCCYLGNKP"
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to residues 1 to 739 of 739 from Escherichia coli K-12 :
B3551"
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/function="putative enzyme; Not classified"
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'fb xref="GI:30043434"
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complement(6845. .7408)
/gene="tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus tag="S4185"
complement(6408, .6848)
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7566. _8264
/gene="yhjY"
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|qene="VhiY"
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Best Local Similarity
Matches 25; Conserv
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/note="Residues 1 to 199 of 199 are 99.49 pct identical to
residues 1 to 199 of 199 from Escherichia coli K-12 Strain
MG1655: B3506"
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GRLLARQSGFLDPVNYRNHFVTILGTIQGEQPGPINKVPYNFLEVNMQGIQVWHLREV
VNYTYNLMDYGYGAFWPEPGWGAPYYTNAVSQVTPELVK"
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ngsycsvppanvslsrkqhqvlscianqmttbbilbklkislktfychkhnimmilnl
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Anotes-No-island #140; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
complement (7845. .8873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon start=1
/transI table=11
product="outer membrane protein induced after carbon
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/gene="chus"
/function="putative transport; Transport of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="sip"
/function="membrane; Cell envelop: Outer membrane
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protein id="AAGS8639.1"
db_xref="G1:12518204"
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/db_xref="GI:12518203"
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6499. .7098
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7254. .7784
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/gene="yhiF"
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/gene="slp"
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Best Local Similarity
Matches 23; Conserv
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//note=Residues 1 to 141 of 141 are 98.58 pct identical to residues 1 to 141 of 141 from Escherichia coli K-12 Strain MG1655: 83503"
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/gane="24907"
/function="orf; Unknown function"
/note="Residues 1 to 249 of 371 are 89.95 pct identical to
residues 1 to 249 of 260 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="menitivanpaccterntlemirnsgteptihytedpetrdeu
VKLiadmgisyrallrknyvepyeelgilaedketrddriidfmlohpilinrpivattig
trlcrpseyvleilpdaokgaptkedgekvydeagkrik"
                                                        /note="Residues 1 to 117 of 117 are 94.87 pct identical to residues 1 to 117 of 117 from Escherichia coli K-12 Strain MG1655: B3501"
                                                                                                                                                                                                                                                                                     /protein_id="AAG58633.1"
| Dax xref="G01:12518198"
| translation="WayEllePIQEWILADETRIGIVLLISEIGELCWCDLCTALDQSO
| prisphlalirasgillidrkQckwyhyrlsphipswaakiiegamrCEQEKVQVIvrn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Residues 1 to 429 of 429 are 100.00 pct identical to residues 8 to 436 of 436 from Escherichia coli K-12 Strain M31655: B3502"
/function="regulator; Protection responses: Drug/analog sensitivity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'function="transport; Protection responses: Drug/analog
                                                                                                                                                                /codon start=1
/transI table=11
/product="transcriptional repressor of chromosomal ars
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/bratef="G1:12518201"
/translation="MLFVGLTGVAHQAILLFTHYSLREIPIIASSMMYQ"
5062. 6177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="arsenical pump membrane protein"
/protein_id="AAGS8634.1"
/db_xref="GI:12518199"
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2707. .3996
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/gene="Z4906"
4546. .4653
/gene="Z4906"
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/transl_table=:
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5062. .6177
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'gene="arsB"
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/gene="arsC"
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/gene="arsC"
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1 (basea 1 to 207991)
Mclaren; S.
                                                                                                                                                                                                                                                                                                                                              Submitted (31-UUL-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Zifah-helpssanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 1, 2003 this sequence version replaced gi:32187728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Center project name: 2212N6
Center project name: 22212N6
Center project name: Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 205928 bases at least Q40
Consensus quality: 206396 bases at least Q30
Consensus quality: 206396 bases at least Q30
Consensus quality: 206396 bases at least Q30
Insert size: 207491; sum-of-contigs
Insert size: 207491; sum-of-contigs
Coverage: 10.18x in Q20 bases; sum-of-contigs Quality
coverage: 10.42x in Q20 bases; agarose-fp
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consists of 6 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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EX545855
BX548855.2 GI:33412513
HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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/organism="Danio rerio"

/mol type="genomic DNA"

/db xref="raxon:7955"

/clone="CH211-212N6"

/clone lib="CH2N1-211"

1. .33257

/note="assembly fragment:00933

fragment chain:1
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fragment_chain:1"
82418. 129660
/note="assembly_fragment:00434
fragment_chain:2"
129761. 140386
/note="assembly_fragment:00494
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Shinagawa, H. Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterchemorrhagic Escherichia coli o157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Makino, X., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S., Kurokawa, K., Ishii, K., Hattori, M., Tatsuno, I., Abe, H., Iida, T., Yamanoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T., Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 Genes Genet. Syst. 74 (5), 227-239 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267888 bp DNA linear BCT 07-MAR-2001
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Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comparative analysis of the whole set of rRNA operons between an enterchemorrhagic Escherichia coli O157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655 Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Escherichia
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futsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
famamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
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Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Hayashi,T., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001) 21156231
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                       Length 207991;
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                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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140487. _185104
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185205. _207991
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clone_end:5P6
vector_side:right"
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190295 TARATCARARACATATRATAR 190319
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Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.0%;
Matches 23; Conservative
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AP002565 BA000007
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PUBMED

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complement (5619. .6623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="wkttgmfptgadpldfthappaselgydgieiwggpphafaddl
kaggirqiralaqtyqmpiigytpetngyptmmtcdremersllwitkladdwkem
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Yipgegkwplrerlmediidrgybgyctvelvtmymneprlyarqalerfrallerde
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to YHFR ECOLI gi 1789776 percent identity 98 in 265 aa (Conserved in E.coli K-12)"
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YHPQ ECOLI gi|1789775 percent identity 98 in 110 aa
(Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative transcriptional regulator"
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                                                                                                                                                        Direct Submission
Submitted (26-UIN-2000) Ken Kurokawa, Osaka University, Genome
Submitted (26-UIN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (B-mail:kenegen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Pax:81-6-6879-2047)
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99 in 462 aa (Conserved in B.coli K-12)"
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                                          5 (bases 1 to 267888)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="identical to YHFL_ECOLI gi|1789770 (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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151_.318
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                                                                                                                                                                                                                                                                                                                                                                                  genome project.
                                                                                                                            Hayashi, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                  REFERENCE
AUTHORS
                                                                                                                                                           TITLE
JOURNAL
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Gaps

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PRI 05-JUN-2003

LOCUS

ACCESSION VERSION XEYWORDS SOURCE

RESULT 11 AL954643

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone ame. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: FMBL; Sw:, SWISSEROT; Tr: TREMEL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the clone part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at the privaw sanger ac.uk/PHGF/Chr.

RP3-384F21 is from the library RPCI-3 constructed by the group of Pitcher information can be found at the proposome 1 may be shorter because we sequence overlapping sections only once, except for a short overlapp. The true right end of clone RP3-384F21 is at 96879 in this sequence. The true right end of clone RP4-809F4 is at 105 in this sequence.
                                                                                                                                                                                                                                                                                                                 HS384F21

Human DNA linear PRI 05-JUN-200

Human DNA sequence from clone RP3-384F21 on chromosome 1q24

Contains probable G protein-coupled receptor, BST, STS, CA repeat, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96879)
Wilkinson, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. Braail enquiries: hunguery@seanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jul 15, 1998 this sequence version replaced gi:2980810.
                               Indels
                               7
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91.7%; Pred. No. 3e+02;
tive 0; Mismatches
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Web site: http://www.sanger.ac.uk
Contact: bumquery@sanger.ac.uk
                                                                                                                                  68091 AAGTCAAAAAGATATATGACTAAA 68114
                                                                                                  2 AAGTCAAAAACATATATGACTTAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL022171.1 GI:3319684
HTG; repeat polymorphism.
Homo gapiens (human)
Homo gapiens
                                   22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
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KEYWORDS
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality; such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mis subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a MAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep RP24-142A19 is from a Male (CSTBL/G1) guouse BAC Library VECTOR: pTARBAC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (26-UN-2003) Wellcome Trust Sanger Institute, Hinxton,
Submitted (26-UN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, Callo 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 27, 2003 this sequence versian replaced gis12131025.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
   /gene="EC84227"
/note="similar to GPH ECOLI gi|1789787 percent identity 99
in 252 aa (Conserved In E.coli K-12)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL954643 11661 bp DNA linear ROD 27-JUN-2003 Wouse DNA sequence from clone RP24-142A19 on chromosome X, complete
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Mammalia; Butheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                 0; Mismatches
                                                                                                                                  Score 21.8; Pred. No. 95;
                                                                                                                                                                                                                                                                                                       163587 TAAGTCAAAACATATATGGTTTAA 163563
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                    1 TAAGTCAAAACATATATGACTTAA 25
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/clone_lib="RPCI-24"
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                                                                                                                                  Query Match
Best Local Similarity 92.0%;
Matches 23; Conservative (
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Query Match

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1875. 15495

18563. 15600

// Note="LiME1 repeat: matches 5515. 6164 of consensus" 15563. 15600

// Note="Li Septement of the consensus" 15793. 15867

// Note="Li repeat: matches 912. 2167 of consensus" 16092. 17228

// Note="Li repeat: matches 912. 2167 of consensus" 17449. 17414

// Note="WIR repeat: matches 67. 260 of consensus" 17449. 17525

// Note="WIR repeat: matches 67. 260 of consensus" 17532. 17565

// Note="WIR repeat: matches 29. 106 of consensus" 17534. 17565

// Note="Missing of the consensus" 17534. 17666

// Note="Missing of the consensus" 17667. 17866

// Note="Alusq repeat: matches 1. 300 of consensus" 17885. 18000

// Note="Li Repeat: matches 638. 760 of consensus" 1888. 18442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.24. .8604

Thote="LiM4 repeat: matches 3562. .4840 of consensus"

1605. .8795

Thote="LiPA2 repeat: matches 5333. .5524 of consensus"

1853. .14099

Thote="LiPA2 repeat: matches 900. .6146 of consensus"

14095. .14874

Thote="LiPA2 repeat: matches 2. .776 of consensus"
                                                                                                                                                                                                                                           3605. .3791
/note="LTR24 repeat: matches 10. .198 of consensus"
3897. .3897
/note="LTR37A repeat: matches 79. ,169 of consensus"
4798. .4935
/note="LTR33 repeat: matches 40. .175 of consensus"
6347. .6840
/note="LTR44 repeat: matches 3050. .3576 of consensus"
6844. .7122
/note="AluSx repeat: matches 3. .280 of consensus"
                                                                                                                                                                                                          217. .3451
note="LTR24 repeat: matches 256. .490 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1384 of consensus"
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omplement(18864. .19338)
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complement (23133. .23589)
/note="match: STS: Em:HSPE79H7"
complement (23950. .24443)
/note="match: GSS: Em:AQ791812"
24438. .24984
                                                                                                    note="AluSg repeat: matches 1. .291 of consensus"
                                                                                                                        1156. .7271

Mote="82 copies 4 mer aaag 75% conserved"

1711. .7316

Mote="73 copies 2 mer ga 69% conserved"
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// note="match: GSS: Em:AQ707236"
20299..2048
// note="L2 repeat: matches 1154..1
20756. .20873
// note="L2 repeat: matches 2631..2
21634..21945
// note="L2 repeat: matches 1767..2
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2401. .22700
                                 /clone="RP3-384F21"
/clone lib="RPCI-3"
256. .542
chromosome="1"
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Inote=Tigger2 repeat: matches 2546. .2707 of consensus"
18599. .39123
                                                                                                                                                                                                                  /note="Aludo repeat: matches 1. .295 of consensus"
28915. .29013 repeat: matches 1. .295 of consensus"
28915. .29013 repeat: matches 17. .114 of consensus"
29185. .29387
/note="MER77 repeat: matches 242. .609 of consensus"
29364. .29387
/note="THEIL repeat: matches 3. .26 of consensus"
30643. .11009
/note="THEIC repeat: matches 1. .371 of consensus"
31381. .31539
/note="TLE repeat: matches 2551. .2738 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40190. .41334
/note="WRRAILA repeat: matches 1. .1266 of consensus"
41340. .42742
/note="11PA16 repeat: matches 3643. .5085 of consensus"
42704. .45055
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                                                                                                                                 'note="PAM repeat: matches 5. .175 of consensus"
[7135. .27382
| note="L1MB8 repeat: matches 5903. .6150 of consensus"
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/note="Tigger2 repeat: matches 1. .327 of consensus"
46749. .47207
/note="match: GSS: Bm:AQ676168"
48122. .48176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2267. .32474
note="MIR repeat: matches 30. .243 of consensus"
2694. .32955
note="L2 repeat: matches 2450. .2710 of consensus"
3042. .33162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="PAM repeat: matches 84. .183 of consensus" 14469. .34641
note="MIR repeat: matches 47. .243 of consensus" 15064. .35363
note="Liz repeat: matches 2410. .2710 of consensus" 15673. .35725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2710 of consensus"
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Indice="4" alusg repeat: matches 1. .310 of consensus" 37715. .37925
Indice="4" alust repeat: matches 3. .245 of consensus" 37926. .37970
Indice="4" alust repeat: matches 2. .50 of consensus" alust repeat: matches 2. .50 of consensus"
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note="18 copies 4 mer tgtg 83% conserved"
4330. .34427
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Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L2 repeat: matches 2588.
4246, .34319
/note="match: GSS: Em:AQ417112"
complement(25242. .25840)
/note="match: GSS: Em:AQ552352"
complement(25484. .26006)
/note="match: GSS: Em:AQ665403"
26767. .26914
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Best Local Similarity 91.7%; Pred. No. 2.8e
Matches 22; Conservative 0; Mismatches
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RESULT 13 AL954640/c DEFINITION ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Anderson, S. (basses to 151950)

Richard, B., Lintcon, L., Nusbaum, C., Lander, B., Abraham, H., Allen, N., Anderson, S. (basses to 151950)

Anderson, S., Barna, N., Barkler, G., Campopiano, M., Castle, A., Choepel, Y., Colangelo, M., Colling, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Colling, S., Collymore, A., Cooke, P., Parkhalter, B. Brown, A., Burkert, G., Campopiano, A., Cooke, P., Parkhalter, C., Campopiano, M., Colling, S., Collymore, A., Cooke, P., Parkeria, P., Cooke, P., Parkeria, P., Cooke, P., Parkeria, C., Dearch, C., Cand-Pierre, N., Bidan, L., Cand-Pierre, N., Barn, L., Karatas, A., LaRocque, K., Inder, T., Olmbron, R., Googe, C., Kam, L., Karatas, A., LaRocque, K., Inder, T., Chonge, C., Kam, L., Karatas, A., Larocque, K., Olong, C., Kam, L., Caratas, R., Meternan, K., Moren, C., Moran, C., Mickernan, K., Moren, C., Peterson, K., Olong, C., Kam, L., Orkell, D., Olong, C., Kam, D., Peterson, K., Olong, C., Kam, C., Peterson, K., Peterson, K., Olong, C., Kam, C., Redore, J., Peterson, K., Olong, C., Kam, C., Redore, J., Struck, S., Schauer, S., Severy, P., Sougez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Struck, S., Schauer, S., Severy, P., Stumer, A., and Zody, M., Santos, R., Schauer, S., Severy, P., Stumer, A., and Zody, M., Travers, M., Triglilo, G., Young, G., Zainoun, J., Milson, B., Mull, S., Challes Street, Cambridge, M. 2011, USA
All repeats were identified using RepeatMasker: thm Center Shemission Canter, Canner Genome Center, Witchead Institute, MIT Center for Genome Research, 320 Charles Street, Cambridge, M. A., Mall, M. S., Submitted (18-NOV-2000) Whitehead Institute, MIT Center for Genome Center: Whitehead Institute, MIT Center for Genome Research, Sound, A., Strojanovi, M., St
151950 bp DNA linear HTG 18-NOV-2000 HOMO sapiens chromosome 8 clone RP11-21H16 map 8, WORKING DRAFT AC084813
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [4 bases 1 to 151950]
Birren, B., Lincon, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-21H16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of 100 bp
contig of 1092 bp in length
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HTG; HTGS PHASE1; HTGS_DRAPT.
HOMO BADiens (human)
HOMO BADIENS
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247:
1339:
                  AC084813/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence was fainished as follows unless otherwise noted: all regions were either double-stranded or sequencing problems, such chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: FMBL; Sw: SWISSROT; Tr: TREMBL; Mp:, WORNPEP; Information on the WORNPEP database can be found at the RPC1-23 Mouse BAC Library constructed by the group of Pieter de Jong.

VECTOR: PBACe2: 300008 BAC Library constructed by the group of Pieter de Jong.

VECTOR: PBACe2: Accession of Pieter de Jong.

VECTOR: PBACe2: Accession of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-53A-2003) Wellcome Trust Sanger Institute, Hinxton, Carbridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Chom on 24, 2003 this sequence version replaced gi:27817477. Sequence from the Mouse Genome Sequencing Consortium Whole genome shotpun may have been used to confirm this sequence. Sequence data from the whole genome shotpun alone has only been used where it has a phied quality of at least 10.
                                                                                                  AL954640 112484 bp DNA linear ROD 24-JAN-2003
Mouse DNA sequence from clone RP23-65C22 on chromosome X, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammālia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
1 (bases 1 to 112484)
Heath,P.
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Web site: http://www.sanger.ac.uk
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1. .112484
                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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RESULT 14

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FEATURES

ORIGIN

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2522 6579: gap of 100 bp
6580 6779: gap of 100 bp
8451 gap of 100 bp
8551 gap of 100 bp
8
econtig of 100 bp

contig of 1454 bp in length

contig of 1025 bp in length

contig of 1025 bp in length

contig of 100 bp

contig of 1133 bp in length

gap of 100 bp
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/clone llb="RPC1-11 Human Male BAC"
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
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AX508952
LOCUS
DEFINITION
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
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Patent: WO 0216655-A 3647 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                               Query Match 80.8%; Score 20.2; DB 6; Length 2000; Best Local Similarity 88.0%; Pred. No. 1e+03; Matches 22; Conservative 0; Mismatches 3; Indels 0;
                                                                  Location/Qualifiers
1. .2000
7. Organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
                                                                                                source
                 JOURNAL
                                                                        FEATURES
                                                                                                                                                                      ORIGIN
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Search completed: May 26, 2004, 17:22:32 Job time : 349.756 secs

1 TAAGTCAAAAACADATATGACTTAA 25 ||| ||| ||| ||||||||| ||| 951 TAAATCATAAACATATATGACATAA 975

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May 26, 2004, 17:50:29 ; Search time 862.256 Seconds (without alignments) 221.574 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ctgcacttacacattcgtta......tcatatatgtttttgactta 42
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| cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US06 PUBW PUB.seq:*
| cgn2 6/ptodata/2/pubpna/US06 PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*
| cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US09A PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US09A PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US09C PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US6O_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2960401 seqs, 2274450654 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-676-299-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		s, Appli	3339, Ap	5, Appli	80, Appl	9, Appli	10, Appl	106547,	229, App	36277, A	36278, A	36279, A	62964, A	62965, A	62966, A
	Description	Sequence 5,	Seguence	Sequence (	Sequence	Sequence	Sequence 1	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Seguence
	ID	US-10-222-952A-5	US-10-282-122A-3339	US-10-222-952A-6	US-10-175-523-80	US-10-222-952A-9	US-10-222-952A-10	US-10-424-599-106547	US-09-997-722-229	US-10-027-632-36277	US-10-027-632-3627B	US-10-027-632-36279	US-10-027-632-62964	US-10-027-632-62965	US-10-027-632-62966
		15	13	15	12	15	15	13	12	13	13	13	13	13	13
	Query Match Length DB	42	401	40	90650	25	25	1494	29956	557	557	557	557	557	557
dР	Ouery Match	100.0	100.0	95.2	61.0	59.5	59.5	59.0	55.7	53.3	53.3	53.3	53.3	53.3	53.3
	Score	42	42	40	25.6	25	25	24.8	23.4	22.4	22.4	22.4	22.4	22.4	22.4
	Result No.	-	0	е С	Ω	Ŋ	9	٥	<b>0</b> 0	O O	c 10	c 11	12	13	14

	36279, 62964, 62965, 62966, 310230 310231		Sequence 4010, Ap Sequence 4010, Ap Sequence 157455, Sequence 157456, Sequence 157456, Sequence 157456, Sequence 157456,
US-10-027-632-310230 US-10-027-632-310231 US-10-027-632-310232 US-10-027-632-3627 US-10-027-632-36278	0-027-632-3627 0-027-632-6296 0-027-632-6296 0-027-632-3102 0-027-632-3102 0-027-632-3102		10-027-632-1554 10-398-221-4010 10-398-221-4010 10-027-632-1574 10-027-632-1574 10-027-632-1574 10-027-632-1574
113	300000000000000000000000000000000000000	9 6 9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	133 199
28.87 78.88 78.88 78.88 78.88	5557 5557 5557 5557 6557 627	1108 11108 11125 11125 11125 11125 11125	9148 8148 771 771 771 771
0.00.00.00 0.00.00.00 0.00.00.00			v v v v v v v v v v v v v v v v v v v
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11 11 11 11 11 11 11 11 11 11 11 11 11		: 00000000 000000000000000000000000000	ი იიიი გ. დ. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.

## ALIGNMENTS

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RESULT I RESULT IS No 102030096278A1

S Sequence 5, Application US/10229528  

S Sequence 5, Application No. US2030096278A1  

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Gaps

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US-1U-IVD-Z2J-80/C
Sequence 80, Application US/10175523
Publication No. US2030096264A1
Sequence 80, Application US-U017503
Publication No. US2030096264A1
SEGUENBAL INPORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: Hook, Derek
APPLICANT: Hook, Derek
APPLICANT: Laeng, Pascal
APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3225/10795-U3
FURENT APPLICATION NUMBER: US 60/299,151
FRIOR APPLICATION NUMBER: US 60/299,151
FRIOR FILING DATE: 2001-06-18
FRIOR FILING DATE: 2001-06-18
FRIOR FILING DATE: 2001-09-07
FRIOR APPLICATION NUMBER: US 60/313,047
FRIOR APPLICATION NUMBER: US 60/313,047
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR APPLICATION NUMBER: US 60/349,936
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR APPLICATION NUMBER: US 60/349,936
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2003-04
FRIOR FILING DATE: 2003-04
FRIOR FILING DATE: 2003-04
FRIOR FRIOR DATE: 2003-04

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                                                                                                                                                                                            Query Match

95.2%; Score 40; DB 15; Length 40;

Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches 40; Conservative 0; Mismatches 0; Indels
                                                                          ; OTHER INFORMATION: CHROMLIB bottom, long oligo sequence
US-10-222-952A-6
                                                                                                                                                                                                                                                                                                                                                                                                                  40 GCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 1
                                                                                                                                                                                                                                                                                                                                                                  3 GCACTTACACATTOGITAAGTCATATATGTTTTTGACTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15;
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Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.0%;
77.5%;
ORGANISM: Artificial Sequence
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CORGANISM: Mus musculus
US-10-175-523-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-175-523-80/c
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: admission.

APPLICANT: Applicant.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REPERROCE: ELITRA. 034A

CURRENT FILING DATE: 2004-02-20

PRIOR PPLICATION NUMBER: 60/191,078

PRIOR PPLICATION NUMBER: 60/206,848

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-26

PRIOR PPLICATION NUMBER: 60/230,335

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PPLICATION NUMBER: 60/253,625

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2000-10-20

PRIOR PRIOR PLING DATE: 2000-10-20

PRIOR PRIOR PLING DATE: 2000-10-20

PRIOR PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR PRIOR PLING DATE: 2001-02-16

PRIOR PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 CTGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 42
                              Rang, Liangsu

Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Mall, Daniel
                                                                                                                                                                                                                                                                                                                      Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Escherichia coli
US-10-282-122A-3339
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LENGTH: 401
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Gaps ö APPLICANT: Regenesis
APPLICANT: Laing, Lance
TITLE OF INVENTION BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REPERENCE: 4107/11443-US.1
CURRENT APPLICATION NUMBER: US/10/222,952A
PRICA APPLICATION NUMBER: US/02-08-15
PRICA PRILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13 66115 CICCACTTATACATTTATACACATATATTATTGACT 66076 1 CTGCACTTACACATTCGTTAAGTCATATATGTTTTTGACT 0; Mismatches Sequence 9, Application US/10222952A Publication No. US20030096275A1 GENERAL INFORMATION: 31; Conservative US-10-222-952A-9 Matches g ਨੇ

Sequence 6, Application US/1022952A
| Sequence 6, Application US/1022952A
| Publication No. US20030096275A1
| GENERAL INFORMATION:
| APPLICANT: Regenesis
| TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
| TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
| FILE REPERBENCE: 4107/1L443.US|
| CURRENT FILING DATE: 2002-0850
| PRIOR APPLICATION NUMBER: US 60/313,714
| PRIOR PLILING DATE: 2002-08-08
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: PALENTIN VERSION 3.1
| SEQ ID NO 6
| TYPE: DNA

Gaps

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NAME/KEY: misc_feature; LOCATION: (29121)..(29589); LOCATION: (29121)..(29589); OTHER INFORMATION: "n" at positions 29121 through 29589 can be any base. US-08-997-72-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36277, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPREMENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KBY: misc feature
LOCATION: (20085)..(20586)
OTHER INFORMATION: "n" at positions 20085 through 20586 can be any
                                                                                                                                                                                                                                                                                           Sequence 259, Application US/09997722

SEQUENCE 259, Application US/09997722

SUBJICATION NO. US20040072154A1

GENERAL INFORMATION:

APPLICANT: MOTINE, David

APPLICANT: MOTINE, David

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REPREBENCE: A.71174/RMS/DCF

CURRENT APPLICATION NUMBER: US/09/997, 722

CURRENT FILING DATE: 2001-11-30

FRIOR FILING DATE: 2001-11-22

FRIOR PELING DATE: 2001-12-22

FRIOR PELING DATE: 2001-03-02

FRIOR FILING DATE: 2001-03-02

FRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 301

SOFTWARE: PALENTIN VETSION 3.1

SEQ ID NO 229

LENGTH: 29956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.7%; Score 23.4; DB 12; Length 29956; Best Local Similarity 73.2%; Pred. No. 4e+02; Matches 30; Conservative 0; Mismatches 11; Indels 0;
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                   DB 13; Length 1494;
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NAME/KEX: misc.
LOCATION: (7091). (7110)
OTHER INFORMATION: "n" at positions 7091 through 7110 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      positions 1335 through 1858 can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEX: misc_feature
LOCATION: (24372)..(24840)
OTHER INFORWATION: "n" at positions 24372 through 24840
                                                                                                                                                                               1332 TAATTCATTCGCTAAATCATATATATTTTCGACTTA 1297
                                                                      7;
                   Query Match 59.0%; Score 24.8; Dest Local Similarity 80.6%; Pred. No. 61; Matches 29; Conservative 0; Mismatches
                                                                                                                            7 TIACACATICGITAAGICATATATGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: {1335}..(1858)
OTHER INFORMATION: "n" at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-027-632-36277/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Avalic David K
APPLICANT: Cao Yongwei
TITLE OF INVERTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVERTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVERTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVERTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 36-21(53223)8
FURBERT APPLICATION NUMBER: US/10/424,599
UURBERT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285564
                                                                                                                               FEATURE:
// OTHER INFORMATION: CHROMS1T top, short biotinylated oligo sequence; biotinylated
// OTHER INFORMATION: nucleotide at position 1
05-10-222-952A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-10-22-952A-10/C
JS-952A-10/C
Sequence 10, Application US/10222952A
Sequence 10, Application No. US20030096275A1
GENERAL INPORMATION:
APPLICANT: Regenesis
APPLICANT: Regenesis
APPLICANT: Regenesis
APPLICANT: Regenesis
APPLICANT: Regenesis
APPLICANT: Negenesis
CURRENT APPLICATION UNMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEX ID NOS: 13
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 10
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

59.5%; Score 25; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                               DB 15; Length 25,
                                                                                                                                                                                                                                                                                                                     0; Indels
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US-10-424-599-106547
                                                                                                                                                                                                                                                            Query Match

S9.5%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches
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SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 25
                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-424-599-106547/c
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LENGTH: 1494
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-36279
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US-1U-U27'-632-46278/C

Publication No. US20020198371A1

GENERAL INCRMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION:

PILE REPERENCE: 108827.12

CURRENT FILING DATE: 108827.12

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR PLING DATE: 2000-07-20

PRIOR PLING DATE: 2000-04-20

PRIOR PLING DATE: 2000-04-20

PRIOR PLING DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 1990-03-29

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-08-09

SOFTWARE FREE FREESEQ for Windows Version 4.0
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Pred. No. 3.4e+02;
0; Mismatches 11; Indels 0;
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           FRIOR APPLICATION WOMBER: US BUJZIB, UUG
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-03
PRIOR PILING DATE: 1999-10-03
PRIOR PILING DATE: 1999-10-03
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASTESEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: 5577
PRIOR APPLICATION NUMBER: US 60/218,006
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Best Local Similarity 72.5%;
Matches 29; Conservative
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US-10-027-632-36278/c
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US-10-027-632-36277
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; ORGANISM: Human
US-10-027-632-36278
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FRIOR FILING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FBSESEQ FOR WINDOWS Version 4.0
SEQ ID NO 62266
LENGTH: 557
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US-10-027-632-310230
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; ORGANISM: Human
US-10-027-632-62966
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US-10-027-632-62966

i Sequence 62966, Application US/10027632

j Sequence 62966, Application US/10027632

j Publication No. US20020198371A1

GENERAL INFORMATION:

j TITLE OF INVEXTION: Identification and Mapping of Single Nucleotide

j TITLE OF INVEXTION: Polymorphisms in the Human Genome

j TITLE OF INVEXTION: Polymorphisms in the Human Genome

j TITLE OF INVEXTION: Polymorphisms in the Human Genome

j FILE REPRENCE: 108827.1139

j CURRENT APPLICATION NUMBER: US 60/198,006

j PRIOR APPLICATION NUMBER: US 60/198,676

j PRIOR FILING DATE: 2000-04-20

j PRIOR FILING DATE: 2000-04-20

j PRIOR FILING DATE: 2000-03-29

j PRIOR APPLICATION NUMBER: US 60/193,483

j PRIOR PILING DATE: 2000-03-29

j PRIOR PILING DATE: 2000-03-29
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                                                                          Score 22.4; DB 13; Length 557;
Pred. No. 3.4e+02;
0; Mismatches 11; Indels 0;
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                                                                  Query Match
Best Local Similarity 72.5
Matches 29; Conservative
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Matches 29; Conser
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ORGANISM: Human
   US-10-027-632-62964
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LENGTH: 557
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US-LUCAZ-54-24-24023

Sequence 310210, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT PILING DATE: 2002-04-30

FRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PLICATION NUMBER: US 60/165,218

PRIOR APPLICATION NUMBER: US 60/165,363

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-108-39

PRIOR PLING DATE: 1999-108-39

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002
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53.3%; Score 22.4; DB 13; Length 557; 72.5%; Pred. No. 3.4e+02; ive 0; Mismatches 11; Indels 0
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Pred. No. 3.4e+02;
0; Mismatches 11; Indels 0
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                                                                                                                                                           2 TGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTT
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Job time : 864.256 secs
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72.5%;
Query Match
Best Local Similarity 72.5
Matches 29; Conservative
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Best Local Similarity 72.5
Matches 29; Conservative
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TAAGTCAAAAACATATATGACTTAACGAATGTGTAAGTGC
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US-10-222-952A-5/c
; Sequence 5, Application US/1022952A
; General No. US20030096275A1
; GENERAL INFORMATION:
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Sequence 3, Appli
Sequence 3139, Ap
Sequence 10, Appl
Sequence 10, Appl
Sequence 206547,
Sequence 216951,
Sequence 216951,
Sequence 599, Appl
Sequence 599, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 117032,
Seguence 117033,
Seguence 117031,
                                                                                                                                                                         (without alignments)
221.574 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1
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                                                                                                                                       May 26, 2004, 17:50:29 ; Search time 821.197 Seconds
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| cgn2 6/ptodata/2/pubpna/US07 PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08 PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08 NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_PUBCCMB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US60_NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-222-952A-6
US-10-222-952A-5
US-10-222-952A-3339
US-10-222-952A-10
US-10-222-952A-10
US-10-222-952A-10
US-10-175-523-80
US-10-175-523-80
US-10-175-523-80
US-10-175-523-80
US-10-175-523-80
US-10-175-523-80
US-10-175-533-117031
US-10-027-632-117033
US-10-027-632-117033
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                                                                                                                                                                                                                                                                                                                                                                                                                        2960401 segs, 2274450654 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Query
Match Length DB
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Maximum DB
                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                                               Run on:
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Sequence 117033,
Sequence 115440,
Sequence 115440,
Sequence 2119, Ap
Sequence 453, App
Sequence 3, Appli
Sequence 36277, A
                                                                                                              Sequence 52964, A Sequence 62966, A Sequence 62966, A Sequence 310231, Sequence 310231, Sequence 36277, A Sequence 36277, A Sequence 62964, A Sequence 62965, A Sequence 62965, A Sequence 62966, A Sequence 62966, A Sequence 52965, A Sequence 52965, A Sequence 62965, A Sequence 52965, A Sequence 52965, A Sequence 52965, A Sequence 52965, A Sequence 310231,
                                                                                                                                                                                                                                                                                                                Sequence 3241, Ap
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Sequence 3241, Ap
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Sequence 4010, Ap
                                                                                                                                                                                                                                                                                          Sequence 310232,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Application US/1022952A
Sequence Application US/1022952A
Fublication No. US20030096275A1
GENERAL INFORMATION:
APPLICANT: Regenesis
APPLICANT: Laing Lance
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REFERENCE: 4107/11.443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
FILE APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 13
SOUTHARRE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
, OTHER INFORMATION: CHROMLIB bottom, long oligo sequence
US-10-222-952A-6
6 US-10-027-632-117032

6 US-10-027-632-115440

10S-10-027-632-115440

10S-10-027-632-115440

10S-10-027-632-1199

10S-10-027-798-453

10S-10-027-798-453

10S-10-027-632-36279

10S-10-027-632-36279

10S-10-027-632-36296

10S-10-027-632-310230

10S-10-027-632-310230
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ORGANISM: Artificial Sequence
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Gaps

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40 40

40;

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) OTHER INFORMATION: CHROMSIT top, short biotinylated oligo sequence; biotinylated; OTHER INFORMATION: nucleotide at position 1
US-10-222-952A-9
                                                                                                                                                                         Gaps
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APPLICANT: Regenesis
APPLICANT: Laing Lance
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REPERENCE: 4107/11443-US1
CURRENT PILITE DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR APPLICATION NUMBER: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 15; Length 25;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25;
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CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR PILLING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3:1
LENGTH: 25
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US-10-222-952A-10
                                                                                                                                                                                                                                                   104 TAAGTCAAAAACATATATGACTTAACGAATGTGTAAGTGC 143
                                                                                                                                                                                                                         1 TAAGTCAAAAACATATATGACTTAACGAATGTGTAAGTGC
                                                                                                                         Score 40; DB 13;
Pred. No. 0.0002;
                                                                                                                                                                         0; Mismatches 0;
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100.0%; Pred. No. 19;
tive 0; Mismatches 0
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Publication No. US20030096275A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10222952A Publication No. US20030096275Al GENERAL INFORMATION:
                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 40; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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                          TYPE: DNA
CRGANISM: Escherichia coli
US-10-282-122A-3339
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Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity
Matches 25; Conserval
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  LENGTH: 401
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US-10-222-952A-5
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                       APPLICANT: Laing, Lance FITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 40; Conservative 0; Mismatches 0;
                                                               FILE REPERNCE: 4107/1L443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR PRILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARER: Patentin version 3.1
SSOFTWARER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/1917/078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
APPLICANT: Regenesis
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| Sequence 216951, Application US/10027632
| Sequence 216951, Application No. US2002018371A1
| Publication No. US2002018371A1
| GENERAL INFORMATION:
| APPLICATI'R Wang, David G
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: IDENTICATION NUMBER: US/10/027,632
| CURRENT APPLICATION NUMBER: US 60/218,006
| PRIOR PILLING DATE: 2000-07-12
| PRIOR PILLING DATE: 2000-04-20
| PRIOR PILLING DATE: 2000-04-20
| PRIOR PILLING DATE: 2000-04-20
| PRIOR PILLING DATE: 2000-03-29
| PRIOR PILLING DATE: 2000-03-29
| PRIOR PILLING DATE: 2000-03-29
| PRIOR PILLING DATE: 1999-11-23
| PRIOR PILLING DATE: 1999-11-23
| PRIOR PILLING DATE: 1999-09-28
| PRIOR PILLING DATE: 1999-09-28
| PRIOR PILLING DATE: 1999-09-28
| PRIOR PILLING DATE: 1999-08-09
| SOFTWARE: PASISED for Windows Version 4.0
| SEQ ID NO 216951
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Dolymorphisms in the Human Genome

TITLE OF INVENTION: 108927.129

TITLE OF INVENTION: 108927.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2000-04-30

PRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-11-23
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          Length 90650;
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                                                                            Indels
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                                                                                                                                                                                                     66076 AGTCAATAATATGTGTATAACAATGTATAAGTG 66112
   Score 24.2; DB 15;
Pred. No. 2.4e+02;
0; Mismatches 8;
                                                                                                                                       3 AGTCAAAACATATATGACTTAACGAATGTGTAAGTG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.5%; Score 22.2; DB 13; 77.1%; Pred. No. 3.8e+02; ive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 AAGTCAGAAAATATATAAATAAAAGACTGGGTAA 390
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; Sequence 216951, Application US/10027632
; Publication No. US20030204075A9
          60.5%;
ilarity 78.4%;
Conservative
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          Query Match
Best Local Similarity
Matches 29; Conserva
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Matches 27; Conserv
                                                                                                                                                                                                                                                                                                       RESULT 8
US-10-027-632-216951/c
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Sovalic David X
APPLICANT: Scoulce David X
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21[51223]8
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 106547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Brockman, Jeirrey
APPLICANT: Brockman, Jeirrey
APPLICANT: Brock, Derek
APPLICANT: Leany, Parian
APPLICANT: Leany, Parian
APPLICANT: Palfreyman, Michael
APPLICANT: Palfreyman, Michael
APPLICANT: Palfreyman, Michael
APPLICANT: Palfreyman, Millan-Parian
APPLICANT: Palfreyman, Millan-Paramerer High THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/1J795-US3
CURRENT PILING DATE: 2002-06-18
FILE REFERENCE: 2325/1J795-US3
CURRENT PILING DATE: 2001-06-18
FRIOR APPLICATION NUMBER: US 60/399,151
FRIOR FILING DATE: 2001-09-06-18
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-01-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TAAGTCAAAACATATATGACTTAACGAATGTGTAA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 62.0%; Score 24.8; D
Best Local Similarity 80.6%; Pred. No. 58;
Matches 29; Conservative 0; Mismatches
TAAGTCAAAACATATATGACTTAA 25
                                                                            1 TAAGTCAAAACATATATGACTTAA 25
                                                                                                                                                                                                                                     Sequence 106547, Application US/10424599 Publication No. US20640031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/10175523
Publication No. US20030096264A1
GENERAL INPORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, David
APPLICANT: Hook, Derek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Mus musculus
US-10-175-523-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                         US-10-424-599-106547
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LENGTH: 90650
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US-10-175-523-80
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Publication No. US20020198371A1

GENERAL INPORMATION:
APPLICANT' Mang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PILING DATE: 2002-04-30
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-30
PRIOR PLING DATE: 2000-04-30
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-11-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1065 AATACACAAACAAATATGGCTTTCCAGATGTGTAAG 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 54.0%; Score 21.6; DB 13; Best Local Similarity 75.0%; Pred. No. 7.2e+02; Matches 27; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AAGTCAAAAACATATATGACTTAACGAATGTGTAAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AAGTCAAAAACATATATGACTTAACGAATGTGTAAG 37
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 1000-03-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-09
NUMBER: OF SEQ ID NOS: 325720
SEQ ID NO 117031
LENGTH.: 1125
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SCOTTARE: FastSEQ for Windows Version 4.0
SEQ ID NO 117032
LENGTH: 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: (11...(1125)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-117031
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Best Local Similarity 75.09
Matches 27, Conservative
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US-10-027-632-117032
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIREPRENEOCK, Christian
APPLICANT: BIRLIN, Kurt
FILIS OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
FILIS EFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: PCT/PP01/07537
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR FILING DATE: 2000-06-30
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-09-01
SRIOR FILING DATE: 2000-09-01
SEQ ID NO 599
LEMENTH: 19082
LEMENTH: 19082
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.12
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                                                                                                                                                                                     Score 22.2; DB 16;
Pred. No. 3.8e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 54.5%; Score 21.8; DB 15; Best Local Similarity 78.8%; Pred. No. 1.2e+03; Matches 26; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 AAGTCAGAAAATATATAATAAAAAGACTGGGTAA 390
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  PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09-09
NUMBER OF SEQ ID NOS: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FABLESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 216951
LENGTH: 611
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Sequence 117031, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 599, Application US/10311455 Publication No. US20030143606A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     Query Match 55.5%;
Best Local Similarity 77.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-216951
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Job time : 821.197 secs
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FEATURE:
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Publication No. US2030204075A9

GREEAL INFORMATION:

APPLICANT: Wang, David G.

ITILE OF INVENTION: Polymorphisms in the Human Genome

ITILE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR PRILING DATE: 2000-07-12

PRIOR PLILING DATE: 2000-07-12

PRIOR PLILING DATE: 2000-07-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLILING DATE: 1900-03-29

PRIOR PLILING DATE: 1900-02-28

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                 US-10-027-622-11033, Application US/10027632

Publication No. US20020193371A1

GENERAL PROFMATION:

APPLICAMT: Wang, David G.

TITLE OF INVENTION:

TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108027.129

CURRENT FILING DATE: 2002-04-30

FRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PRIOR FILING DATE: 2000-07-29

PRIOR PRIOR FILING DATE: 2000-03-29

PRIOR PRIING DATE: 2000-03-29

PRIOR PRIING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR PRIING DATE: 1999-11-23

PRIOR PRING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

PRIOR PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR PRIOR FILING DATE: 1999-09-08-09

PRIOR PRIOR FILING DATE: 1999-09-08-09

PRIOR PRIOR FILING DATE: 1999-09-08-09
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Best Local Similarity 75.0%; Pred. No. 7.2e+02;
Matches 27; Conservative 0; Mismatches 9; Indels 0;
1065 AATACACAAACAAATATGGCTTTCCAGATGTGTAAG 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(1125)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-117033
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LENGTH: 1125
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US-10-027-632-117032

| Sequence 117032, Application US/10027632
| Sequence 117032, Application US/10027632
| Publication No. US20030204075A9
| GENERAL INFORMATION:
| TITLE OF INVENTION: 104027.129
| TITLE OF INVENTION: 104027.129
| CURRENT PILING DATE: 2002-04-30
| PRIOR PELICATION NUMBER: US/10/027,632
| CURRENT PILING DATE: 2000-07-18,676
| PRIOR APPLICATION NUMBER: US 60/19,066
| PRIOR APPLICATION NUMBER: US 60/19,666
| PRIOR PILING DATE: 2000-04-20
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/193,383
| PRIOR APPLICATION NUMBER: US 60/195,218
| PRIOR APPLICATION NUMBER: US 60/156,358
| PRIOR APPLICATION NUMBER: US 60/156,363
| PRIOR APPLICATION NUMBER: US 60/146,002
| PRIOR PILING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-09-09-09
| NUMBER OF SEQ ID NOS: 325720
| SEQ ID NO 117032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.0%; Score 21.6, DB 16; Best Local Similarity 75.0%; Pred. No. 7.2e+02; Matches 27; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AAGTCAAAACATATATGACTTAACGAATGTGTAAG 37
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 117031
LENGTH: 1125
LENGTH: 1125
CYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                          FRATURE:
| FRATURE:
| NAME/KEY: misc feature
| LOCATION: (1)...(1125)
| OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-117032
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Sequence 11, Appl Sequence 1995, Appl Sequence 1, Appl Sequence 119, Appl Sequence 1119, Appl Sequence 115, Appl Sequence 115, Appl Sequence 3794, Appl Sequence 119, Appl Sequence 1, Appl Sequence 9, Appl Sequence 1, Appl Sequence 2280, Appl Sequence 2280, Appl Sequence 1, Appl
                                                                                                                                                                                                                                May 26, 2004, 16:18:00; Search time 36.6624 Seconds (without alignments) 348.146 Million cell updates/sec
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Sequence 98
Sequence 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-136-135-119

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US-09-116-283-9

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US-09-10-532A-765

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US-09-116-43-9

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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 41, Application US/09596002
Farent No. 6632636
GENERAL INFORMATION:
APPLICANT: Lagace, Robert, B.
APPLICANT: Berg.
APPLICANT: PEPRICANT: APPLICANT: APPLICAN
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1177, App
174, App
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662, App
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2378, App
17, Appl
1890, App
1890, App
254, Appl
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1189, Ap
1, Appli
178, App
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Sequence 10, Appl
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANIEM: Moraxella catarrhalis
PERATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID No. 6632636 41
19811CATION INFORMATION:
                         US-09-060-756-174
US-09-670-314-174
US-09-670-314-662
US-09-570-314-662
US-09-543-681A-17
US-09-543-681A-17
US-08-543-794-1
US-08-540-236-1890
US-09-540-236-1890
US-09-711-164-254
US-09-711-188-67
US-09-148-581D-1
US-08-148-581D-1
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US-08-148-581D-1
US-08-148-581D-1
US-08-53-313D-178
US-08-58-910-1
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Best Local Similarity 90.9
Matches 20, Conservative
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Sequence 1995, Application US/09134001C

Sequence 1995, Application US/09134001C

Batent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERABEUTICS

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERABEUTICS

FILE REPERENCE: GT-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998=08-13

FRIOR FILING DATE: 1997-11-08

FRIOR FILING DATE: 1997-11-08

FRIOR FILING DATE: 1997-11-08

FRIOR FILING DATE: 1997-10-08-14

RESULT 2 US-09-134-001C-1995/c

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GENERAL INFORMATION:
    Patent No. 6528289
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                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
Thereof, and Uses Thereof
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                          DB 4; Length 1026;
                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: I CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Deal Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATE: 0.09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: OFFENDON
PRIOR APPLICATION: OUMBER: 08/476,102
FILING DATE: 35-Apr-2000
CLASSIFICATION: OUMBER: 08/476,102
FILING DATE: 0.00-2.195
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REFERENCE/DOCKET NUMBER: 41,971
REFERENCE/DOCKET NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186F3
TELECOMMUNICATION INFORMATION:
TELEPONE: 301-309-8504
TELEPAX: 301-309-8439
INFORMATION FOR SEQ. 11.
                                                                                                                                        Query Match 79.1%; Score 18.2; I Best Local Similarity 87.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches
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90.5%; Pred. No. 39; [
cive 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                              ORGANISM: Staphylococcus epidermidis US-09-134-001C-1995
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LENGTH: 1830121 base pairs
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Best Local Similarity 90.5
Matches 19; Conservative
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1995
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ZIP: 20850
                                         LENGTH: 1026
TYPE: DNA
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RESULT 4 US-09-643-990A-1/c . Sequence 1, Application US/09643990A

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Patent No. 6605709
Sequence 1519, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1519
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                                                           Hamilton O. Smith
J. Craig Venter
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 1830121;
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                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGNT INFORMATION:
NAME: REPERENCE/DOCKET NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186FIC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.4%; Score 17.8; I 90.5%; Pred. No. 39; tive 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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APPLICANT: Robert D. Fleischmann
Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AATCATATGCGTTTTTGGTTA 23
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS
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Best Local Similarity 90.5'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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Sequence 300, Application US/09328352
Sequence 300, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BADANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION WUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 300
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| Patent No. 6617156 |
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| Patent No. 6617156 |
| General Information |
| Patent No. 6617156 |
| General Information |
| TITLE OF INVERTION |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
72.2%; Score 16.6; D
Best Local Similarity 82.6%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches
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1 ORGANISM: Acinetobacter baumannii

US-09-328-352-300
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ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Enterococcus faecalis
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les 19, Conserv
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US-09-134-000C-724
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   RESULT 8
US-09-328-352-300
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Matches
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Patent No. 6605709
GENERAL INFORMATION:
TITLE OF INVENTION: UDGGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1200-04-05
PRIOR FILING DATE: 1999-04-09
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US-09-669-751-43/C

US-09-669-751-43/C

US-09-669-751-43/C

Sequence 43. Application US/09669751

TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Balance and the Perception of Gravity

FILE REFERENCE: P-NI 3864

CURRENT FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US 60/168,579

PRIOR FILING DATE: 1999-12-02

NUMBER OF ED ID NOS: 261

SOFTWARE: PRASEC for Windows Version 4.0
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                                                                                                                  Score 17.4; DB 4; Length 1386; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.8%; Score 17.2; DB 4; Length 627; 86.4%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 678;
                                                                                                                                                                            i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                      422 rradicciardcerritic 440
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                                                                                                                                                                                                                                  TTG 19
                                                                                                                  75.7%;
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Best Local Similarity 90.0%;
Matches 18; Conservative
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Proteus mirabilis
US-09-543-681A-815
                                                                                                               Query Match
Best Local Similarity 94.7
Matches 18; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Conservative
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SEQ ID NO 815
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-09-543-681A-815/c
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LENGTH: 627
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TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-790-988-1/c
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Sequence 41, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

ITILE OF INVENTION: Dy Assessing DNA Methylation

FILE REPERENCE: 5013-1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT PILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98
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                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Boksberg, Leonard, N.
APPLICANT: Bubbers, Mark W.
APPLICANT: Lubbers, James
APPLICANT: Orker, James
APPLICANT: Gristensson, Anna C.
APPLICANT: Gristensson, Anna C.
APPLICANT: Grid, Julian R.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: them and methods for using them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                         72.2%; Score 16.6; DB 4; Length 2235; 82.6%; Pred. No. 79; 1ve 0; Mismatches 4; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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82.6%; Pred. No. 88;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
                                                                                                                                                        1214 TCAATCAATGCATTTTTGGTAA 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4323 TAAAGCATTTGCGATTTTGGTTA 4301
                                                                                                                                 1 TTAATCATATGCGTTTTTGGTTA 23
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                                                                                                                                                                                                                                                                            Sequence 15, Application US/09634238 Patent No. 6544772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Lactobacillus rhamnosus US-09-634-238-15
                                         Query Match
Best Local Similarity 82.63
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.6
Matches 19; Conservative
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US-09-634-238-15/c
US-09-328-352-3794
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LENGIH: 7210
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Pred. No. 1.2e+02;
0; Mismatches 4; Indels 0;
FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-41
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                                                                     Length 8537;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION: 123 Human Secreted Proteins TITLE OF INVENTION: 123 Human Secreted Proteins TITLE OF INVENTION: 123 Human Secreted Proteins TITLE OF INVENTION: 123 Human Secreted Proteins CORRENT APPLICATION NUMBER: US/09/227,357 CURRENT FILING DATE: 1999-01-08 EARLIER FILING DATE: 1998-07-07 EARLIER PILING DATE: 1997-07-08 EARLIER PILING DATE: 1997-07-08 EARLIER FILING DATE: 1997-07-08 EARLIER PLING DATE: 1997-07-08 EARLIER PLING DATE: 1997-07-08 EARLIER PLING DATE: 1997-07-08
                                                                           DB 4;
                                                                         Score 16.6; D
Pred. No. 89;
0; Mismatches
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/052,803
FILING DATE: 1997-07-08
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Patent No. 6342581
                                                                                                                                                       1 TTAATCATATGOGFTTTTGGTTA
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                                                                         Query Match 72.2%;
Best Local Similarity 82.6%;
Matches 19; Conservative
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Best Local Similarity 82.6%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTAATCATATGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Buchnera sp.
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750 TAATCATATTTGTTTATGGTT 770

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Query Match 70.4%; Score 16.2; DB 4; Length 1442; Best Local Similarity 85.7%; Pred. No. 1.2e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-08-18
EARLIER FILING D
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OTHER INFORMATION: n equals a,t,g, or C
FEATURE:
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) OTHER INFORMATION: n equals a,t,g, or c

US-09-227-357-119
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ORGANISM: Homo sapiens
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RESULT 15
US-084-9
US-08-472-028A-9
| Sequence 9, Application US/08472028A|
| Patent No. 5767373|
| GANERAL INFORMATION:
| APPLICANT: Wolrath, Sandra |
| TITLE OF INVENTION: Manipulation of Protoporphyrinogen |
| TITLE OF INVENTION: Oxidase Bnzyme Activity in Eukaryotic Organisms |
| WUMBER OF SEQUENCES: 12 |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Capacition |
| STREET: 7 Skyline Drive |
| CITY: Hawthorne |
| STATE: NY |
| STATE: NY |
| COUNTRY: USA |
| COUNTRY: USA |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.4%; Score 16.2; DB 1; Length 1697; Best Local Similarity 85.7%; Pred. No. 1.2e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 29..1501
OTHER INFORMATION: /note= "Arabidopsis protox-3 cDNA;
OTHER INFORMATION: sequence from pMDC-5"
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USAL
ZIP: 10522
COMPUTER 10522
COMPUTER PLOEDY disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/472,028A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Elear, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1748/CIP
TELECOMMUTICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEPHONE: 919-541-8614
TELEPHONE: 199-541-8619
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1697 Dase pairs
TWOR: nucleic acid
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STRANDEDNESS: sing
TOPOLOGY: linear
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HYPOTHETICAL: NC
ANTI-SENSE: NO
FEATURE:
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Gaps

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Sequence 7, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 41, Appli
Sequence 10855, A
Sequence 10855, A
Sequence 10855, A
Sequence 10851, A
Sequence 1667, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2257, Ap
                                                                                                                      May 26, 2004, 17:50:29; Search time 472.188 Seconds (without alignments) 221.574 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/DS07_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 US-10-329-960-1
5 US-10-329-670-1
US-10-282-122A-32597
US-10-255-536-43
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5 US-10-222-952A-3

10-10-222-952A-4

5 US-10-222-952A-4

6 US-10-094-749-622

3 US-10-672-707-41

US-09-867-701-10855

3 US-10-424-589-90942

6 US-10-313-650-167
                                                                                                                                                                                                                                                                                                                                                                                                    fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                           2960401 seqs, 2274450654 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                     1 ttaatcatatgcgtttttggtta 23
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                              IDBNTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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100.0 30
91.3 28
81.7 26923
79.1 505
77.4 2675
77.4 10717
77.4 1870121
77.4 1830121
77.4 1830121
77.4 1830121
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                             :10
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TTAATCATATGCGTTTTTGGTTA 23

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RESULT 2 US-10-222-952A-3 Sequence 3, Application US/10222952A Publication No. US20030096275A1

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Gaps
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                                                                                                                                                                                                                              Length 28;
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                                                                                                                                                            CTHER INFORMATION: PLASLIB bottom, long oligo sequence US-10-222-952A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18.8; DB 16;
Pred. No. 3.6e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                           DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SEKI, NAGHIKO
APPLICANT: SEKI, NAGHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHAI, KENJI
APPLICANT: NAGAHAI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILER REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT PILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
                                                                                                                                                                                                                           91.3%; Score 21; DB 100.0%; Pred. No. 20; ive 0; Mismatches
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; Sequence 41, Application US/10672787
; Publication No. US20040067554A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  3 AATCATATGCGTTTTTGGTTA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUGI
APPLICANT: WAKAMATSU, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative
                  NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 28
                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAMBCHIKA, ICHIRO
PRIOR FILING DATE: 2001-08-20
                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.1
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHIZUKO
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CORGANISM: Homo sapiens
US-10-094-749-622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTSUKA,
NAGAI, K
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-094-749-622/c
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LENGTH: 3727
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                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: PLASLIT biotinylated top, long oligo sequence; biotinylated OTHER INFORMATION: nucleotide at position 1
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Publication No. US2000096275A1;
GENERAL INFORMATION:
APPLICANT: Regenesis
APPLICANT: Lairg, Lance
TITLE OF INVENTION: BIOSENSOR FOR SWALL MOLECULE ANALYTES
FILE REFERENCE: 4107/11443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR PILING DATE: 2001-08-20
NUMBER OF SEQ ID NGS: 13
SOFTHARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 23; DB 15; Length 30; Best Local Similarity 100.0%; Pred. No. 2.9; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
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                                        APPLICANT: Laing, Lance
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REPERENCE: 410/11443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR PAPLICATION NUMBER: US 60/313,714
PRIOR PAPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NOS: 13
LENGTH: 30
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APPLICANT: Laing. Lance
APPLICANT: Laing. Lance
APPLICANT: Laing. Lance
FILLE REPERENCE: 4107/1L43-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGTTA 23
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                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TIAATCATAIGCGTTT
                      APPLICANT: Regenesis
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US-10-222-952A-4/c
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Sequence 1667, Application US/10311455
Sequence 1667, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                   Score 17.8; DB 13;
Pred. No. 6.9e+02;
0; Mismatches 2;
    ; TYPE: DNA;
; ORGANISM: Glycine max;
; FRATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53131C.1
US-10-424-599-90942
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CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US /10/383,630
PRIOR PILING DATE: 2002-03-27
PRIOR PILING DATE: 2002-03-27
PRIOR PILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KODAMA, HIROSHI
APPLICANT: WADA, YASUNAO
APPLICANT: SHIKAFA, SHITSU
APPLICANT: STAKAFA, SHITSU
APPLICANT: TITLE OF INVENTION: Mutant alkali cellulase
FILE REFERENCE: 234890US0
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Publication No. US20040002431A1
GENERAL INFORMATION:
APPLICANT: HAKAMADA, YOSHIHIRO
APPLICANT: SAWADA, KAZUHISA
APPLICANT: ENDO, KEIJI
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                                                                                                                                                                                                                                                                   Match 77.4%;
Local Similarity 90.5%;
les 19; Conservative
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| OTHER INFORMATION:
US-10-383-630-1
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US-10-311-455-1667
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                                                                                                                                                                                                                                                                            Query Match
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Matches
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Toou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERENCE: 38-21(5323) and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323) and Uses Thereof for Plant Improvement
CURRENT PLILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 90942
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APPLICANT: LAGACE, Robert, E.
APPLICANT: PATTERSON, Chandra
APPLICANT: PATTERSON, Chandra
APPLICANT: PATTERSON, CHANGRA
APPLICANT: BERG, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REPERENCE: ELITRAY 0.25C1
CURRENT APPLICATION NUMBER: US/10/672,787
CURRENT FILING DATE: 2003-09-26
PRIOR FILING DATE: 2000-66-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE PERL PROGRAM
SEQ ID NO 41
LENGTH: 269223
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Sequence 10855, Application US/09867701

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1. Similarity 90.9%; Pred. No. 6.8e+02;
20; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-10-672-787-41
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CORGANISM: Homo sapien
US-09-867-701-10855
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Best Local Similarity
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US-09-867-701-10855
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US-10-424-599-90942
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NAME/KEY: misc_feature
LCCATION: (51805)..(51805)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (45533)..(45593)
OTHER INFORMATION: n equals a, t,
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LOCATION: (51334)..(51334)

OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a,
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MAKE/KRY: misc_feature
LOCATION: (51602)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a,
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LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a,
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,
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LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a,
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals a,
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (100091)
OTHER_INFORMATION: n equals a,
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a,
            LOCATION: (40808).,(40810)
OTHER INFORMATION: n equals a,
                                                                                                NAME/KEY: misc_feature
LOCATION: (44416)
OTHER INFORMATION: n equals a,
FEATURE:
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LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (107248)..(107248)
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LOCATION: (102596)..(102696)
OTHER INFORMATION: n equals
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; Sequence 1, Application US/10329960
; Publication No. US2003009277A1
; GENERAL INFORMATION:
    APPLICAMT: Fleischmann et al.
    APPLICAMT: Fleischmann et al.
    APPLICAMT: Fleischmann et al.
    TITLE OF INVENTION: Thereof, and Uses Thereof
    TITLE OF INVENTION: UNMERR: US 09/643,990
    PRIOR PILING DATE: 2000-08-23
    PRIOR PILING DATE: 1995-06-07
    PRIO
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                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1667
                                                                                                                                                                                                                                                                                                                           Query Match
77.4%; Score 17.8; DB 15; Length 10717;
Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (36636)..(36636)
OTHER INFORWATION: n equals a, t, g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals a, t, g or or prature:
LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals a, t, g or
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1667
LENGTH: 10717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4757 TTAATTAGATGCGTTTTTGGT 4777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRATURE:
NAME/KEY: misc feature
LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a, t, g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAMEN KEXT: misc feature
LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a, t, g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTAATCATATGCGTTTTTTGGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (36543)...(36543)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (36551)...(36551)
OTHER INFORMATION: n equals a,
                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-10-329-960-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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OTHER INFORMATION: n equals a, t, g

RESULT 12

US-10-329-670-1/C

US-10-329-670-1/C

Sequence 1, Application US/10329670

Publication No. US20040018503A1

GENERAL INFORMATION:

APPLICATION NUCLEOCIDE Sequence of the Haemophilus influenzae Rd Genome, Fra

TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: UNMERR: US 09/643,990

PRIOR FILING DATE: 2000-08-23

PRIOR FILING DATE: 1995-06-07

PRIOR PLING DATE: 1995-06-07

PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH 1830121 ö Gaps Length 1830121; ö 2; Indels Query Match 77.4%; Score 17.8; DB 15; Best Local Similarity 90.5%; Pred. No. 1.5e+03; Matches 19; Conservative 0; Mismatches 2; υ O O Ų 1238911 AACAATATGCGTTTTTGGTTA 1238891 ö ö ğ FEATURE:
NAME/KEY: misc feature
LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals a, t, g or
FEATURE:
NAME/KEY: misc feature
LOCATION: (9921)...(9921)
OTHER INFORMATION: n equals a, t, g or å ö ö ö ö FRATURE:
NAME/KEY: misc\_feature
LCARIKEY: (44416). (44416)
OTHER INFORMATION: n equals a, t, g ø ģι ρ b Ø 3 AATCATATGCGTTTTTGGTTA 23 PEATURE:
NAME/KEY: misc\_feature
LOCATION: (36543)...(36543)
OTHER INFORMATION: n equals a, t, TYPE: DNA ORGANISM: Haemophilus influenzae NAME/KEY: misc feature LOCATION: (29298)..(29298) OTHER INPORMATION: n equals a, NAME/KEY: misc feature LOCATION: (40808)..(40810) OTHER INFORMATION: n equals a, PEATURE:
NAME/KRY: misc\_feature
LOCATION: (36551). (36551)
OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (36636)..(36636) OOTHER INFORMATION: n equals a, FEATURE: FEATURE: NAME/KEY: misc feature LOCATION: (152530)..(152530) FRATURE:
NAME/KEY: misc feature
LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals FEATURE FRATURE g δ

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Thu May 27 10:11:46 2004

NAME/KEY: misc feature LOCATION: (117136)..(117136) OTHER INFORMATION: n equals a, t, g or c NAME/KEY: misc feature LOCATION: (102595)..(102696) OTHER INFORMATION: n equals a, t, g or c NAME/KEY: misc\_feature LOCATION: (65309)..(65309) OTHER INFORMATION: n equals a, t, g or FEATURE: NAME/KEY: misc feature LOCATION: {65313}..(65313) OTHER INFORMATION: n equals a, t, 9 or ö NAME/KEY: misc feature LOCATION: (51805)..(51805) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (105121)..(105121) OTHER INFORMATION: n equals a, t, 9 NAME/KEY: misc feature LOCATION: (100091)..(100091) OTHER INFORMATION: n equals a, t, g NAME/KEY: misc feature LOCATION: (44975)..(44975) OTHER INFORMATION: n equals a, t, g FEATURE:
NAME/KEY: misc\_feature
LOCATION: (45593)
OTHER INFORMATION: n equals a, t, g NAME/KEY: misc feature LOCATION: (47036)..(47036) OTHER INFORMATION: n equals a, t, g ANE/KEY: misc feature LOCATION: {51602}..(51602) OTHER INFORMATION: n equals a, t, 9 NAME/KEY: misc feature LOCATION: (51786)..(51786) OTHER INFORMATION: n equals a, t, 9 LOCATION: (44905)..(44905) OTHER INFORMATION: n equals a, t, 9 NAMB/KEY: misc feature LOCATION: (80024)..(80024) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (107248)..(107248) OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEY: misc\_feature
LOCATION: (51334).
OTHER INFORMATION: n equals a, NAMES/KEY: misc feature LOCATION: {45732}..(45732) OTHER INFORMATION: n equals a, NAMES/KEY: misc feature LOCATION: (55369)..(55369) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc\_feature NAMB/KEY: misc feature LOCATION: (44905)..(44)

Gaps Query Match 77.4%; Score 17.8; DB 16; Length 1830121; Best Local Similarity 90.5%; Pred. No. 1.56+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; G FEATURE:
NAME/KEY: misc\_feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a, t, g or c NAME/KEY: misc\_feature LOCATION: (150841)..(150841) OTHER INFORMATION: n equals a, t, g or ö or Ģ ģ ö g ö ŏ ö ö 占 Ø σ NAME/KEY: misc feature LOCATION: (142750)..(142750) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (145942)..(145942) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (122167)...(122167) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (131360)..(131360) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (145171)..(145171) OTHER INFORMATION: n equals a, t, LOCATION: (119750)..(119750) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (147197)..(147197) OTHER INFORMATION: n equals a, FRATURE:
NAME/KEY: misc feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (119924)..(119924) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (121344)..(121344) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (122336)..(122336) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (131340)..(131340) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (139910)..(139910) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (140398)...(140398) OTHER INFORMATION: n equals a, FEATURE:
NAME/KEY: misc feature
LOCATION: (145058)
OTHER INFORMATION: n equals a, FEATURE: NAME/KEY: misc feature LOCATION: (152530)..(152530)

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Balance and the Perception of Gravity 3864
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US-10-255-536-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-10-027-632-202848/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Publication No. US20030087807A1;
GENERAL INFORMATION:
- APPLICANT: Greenspan, Ralph J.
- TITLE OF INVENTION: Methods for Identifying Compounds for INVENTION: Methods for INTLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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TITLE OF INVENTION: Identification of Bssential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT PLING DATE: 2003-02-20
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/291,078
PRIOR PELICATION NUMBER: 60/200,727
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 32597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                               1238911 AACAATATGCGTTTTTGGTTA 1238891
                                                                                                                                                                                                                         Sequence 32597, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRAICATATGCGITTITG 19
                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPB: DNA
; ORGANISM: Proteus mirabilis
US-10-282-122A-32597
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.7
Matches 18; Conservative
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US-10-255-536-43/c
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPREBRENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRICE APPLICATION NUMBER: US 60/198,676
FRICE FILING DATE: 2000-05-20
FRICE PRICE PRICE 2000-05-20
FRICE PRICE PRICE 2000-05-20
FRICE PRICE PRICE 2000-05-29
FRICE PRICE PRICE 2000-05-29
FRICE FILING DATE: 2000-05-29
FRICE FILING DATE: 1999-09-28
FRICE FILING DATE: 1999-09-28
FRICE FILING DATE: 1999-09-28
FRICE FILING DATE: 1999-09-08
FRICE FILING DATE: 1999-09-08
FRICE FILING DATE: 1999-08-09
FRICE F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.8%; Score 17.2; DB 15;
86.4%; Pred. No. 1.3e+03;
Live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
74.8%; Score 17.2; DB 13;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4;
TITLE OF INVENTION: Balance and the Percept:
FILE REFERENCE: P-NI 3864
CURRENT APPLICATION NUMBER: US/10/255,536
CURRENT FILING DATE: 2002-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 1090-12-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 261
SOFTWARE: PSECSEE FOR WINDOWS VERSION 4.0
SOFTWARE: PSECSEE
LENGTH: 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 202848, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 27, 2004, 06:16:38 Job time : 491.188 secs
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Best Local Similarity 86.4
Matches 19; Conservative
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us-10-676-299-7.rnpb

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Sequence 7, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 22, Appl
Sequence 30942, A
Sequence 31760, A
Sequence 228, Appl
Sequence 41, Appli
Sequence 143, Appli
Sequence 1433, Appli
Sequence 1433, Appli
Sequence 1433, Appli
Sequence 1433, Appli
                                                                                              May 26, 2004, 17:50:29; Search time 431.128 Seconds (without alignments) 221.574 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications NA:*

| cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/PCT_MBW_BUB.seq:*
| cgn2_6/ptodata/2/pubpna/PCT_MBW_BUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                 5920802
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-311-455-228
US-10-672-787-41
US-10-312-841-2
US-10-087-192-1483
US-10-424-599-110156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-222-952A-8
US-10-222-952A-4
US-10-222-952A-3
US-10-222-952A-3
5 US-10-322-950-1
6 US-10-329-960-1
US-10-094-749-622
US-10-424-599-90942
                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                  2960401 seqs, 2274450654 residues
                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - nucleic search, using sw model
                                                                                                                                                                                            1 taaccaaaaacgcatatgatt
                                                                                                                                                                                                                         IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                            US-10-676-299-8
21
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1830121
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                              Title:
Perfect score:
                                                                       OM nucleic
                                                                                                                                                                                               Seguence:
                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                      Run on:
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269223 3673778 33805

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Sequence 218409,
Sequence 3100, Ap
Sequence 3100, Ap
Sequence 3131, Ap
Sequence 3131, App
Sequence 1168, App
Sequence 117, App
Sequence 1181, App
Sequence 1181, App
Sequence 114763,
Sequence 114763,
Sequence 2180, Ap
Sequence 21804, Ap
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Sequence 8, Application US/1022952A

Sequence 8, Application US/1022952A

Publication No. US20030096275A1

GENERAL INFORMATION:

APPLICANT: Regenesis

TITLE CP INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES

TITLE CP INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES

TITLE PRICATION UNMERR: US/10/222,952A

CURRENT APPLICATION UNMERR: US 60/313,714

PRICA APPLICATION UNMERR: US 60/313,714

PRICA PILING DATE: 2001-08-15

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PATENTIN UNMERR: US 60/313,714

SEQ ID NOS: 13

SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: PLASSIB bottom, short oligo sequence
US-10-222-952A-8
          3 US-10-027-652-218409

6 US-10-027-652-218409

1 US-09-938-842A-3670

2 US-10-264-213-15

5 US-10-264-213-15

6 US-10-027-622-174763

1 US-10-027-622-176763

1 US-10-027-622-186434

US-10-027-622-186434

US-10-027-622-186434

US-10-027-622-186434

US-10-027-622-186434

US-10-027-622-186434

US-10-027-622-186434
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US-10-222-952A-7/c
US-10-222-952A-7/c
; Sequence 7, Application US/10222952A
; Publication No. US20030096275A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TAACCAAAACGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAACCAAAACGCATATGATT 21
                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                      325348
580073
2940917
2940917
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TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: PLASLIT biotinylated top, long oligo sequence; biotinylated
OTHER INFORMATION: nucleotide at position 1
US-10-222-952A-3
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                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                Length 30;
                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                              Query Match 100.0%; Score 21; DB 15; Best Local Similarity 100.0%; Pred. No. 5.8; Matches 21; Conservative 0; Mismatches 0;
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
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                                                                                                                                                                                                                                                                                                                        23 TAACCAAAACGCATATGATT 3
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (29298). (29298)
OTHER INFORMATION: n equals a,
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NAME/KRY: misc feature
LOCATION: (9921)...(9921)
OTHER INFORMATION: n equals a,
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (36551)..(36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                   ), OTHER INFORMATION: PLASSIT top, short biotinylated oligo sequence, biotinylated , OTHER INFORMATION: nucleotide at position 1 US-10-222-952A-7
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; Sequence 4, Application US/2030096275A1
; Publication No. US20030096275A1
; GENERAL INFORMATION:
; APPLICANT: Regenesis
; APPLICANT: Laing, Lance
; TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
; FILER REPERENCE: 4107/11443-US1
; CURRENT APPLICATION NUMBER: US 60/313,714
; PRIOR APPLICATION NUMBER: US 60/313,714
; PRIOR APPLICATION NUMBER: US 60/313,714
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SOFTWARE: Patentin version 3.1
; SOFTWARE: Patentin version 3.1
                 APPLICANT: Laing, Lance
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REFERENCE: 4107/11443-US1
CURRENT APPLICATION NUMBER: US 60/313,714
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
IENGTH: 23
TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
FERTURE:
FERTURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 15; Length 28;
Pred. No. 5.8;
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Sequence 3, Application US/1022952A
Enblication No. US20030096275A1
GENERAL INFORMATION:
APPLICANT: Regenesis
APPLICANT: Laing, Lance
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REFERENCE: 4107/L1443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR PILING DATE: 2001-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: PLASLIB bottor, long oligo sequence US-10-222-952A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TAACCAAAAAGGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 TAACCAAAACGCATATGATT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
        APPLICANT: Regenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-10-222-952A-3/c
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us-10-676-299-8.rnpb

NAME/KEY: misc feature
LOCATION: (65309)...(65309)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (65313)...(65313)
OTHER INFORMATION: n equals a, t, g or c
FEATURE: NAME/KEY: misc feature LOCATION: (105121)..(105121) OTHER INFORMATION: n equals a, t, g or c NAME/KEY: misc feature LOCATION: {80024}..(80024) OTHER INFORMATION: n equals a, t, g or c g or c RATURE: (AME/KEY: misc\_feature (ACATION: (51805)..(51805) OTHER INFORMATION: n equals a, t, g or FEATURE: NAME/KEY: misc\_feature LOCATION: (19691)..(10091) OTHER INFORMATION: n equals a, t, g or g or ö FEATURE:
NAME/KRY: misc feature
NAME/KRY: misc feature
OTHER INFORMATION: 0 or 0 or g or AME/KEY: misc feature LOCATION: (47036)...(47036) DTHER INFORMATION: n equals a, t, g or gor t, g or 6 m FEATURE:
NAME/KEY: misc feature
LOCATION: (55369)...(55369)
OTHER INFORMATION: n equals a, t, FEATURE:
MANG/KGY: misc\_feature
LOCAFION: (4553)..(45593)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (44905)..(44905) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (45732)..(45732) OTHER INPORMATION: n equals a, t, FEATURE:
NAME/KEY: misc\_feature
COCATION: (51334). (51334)

7THER INFORMATION: n equals a, t, LOCATION: {40810} OTHER INFORMATION: n equals a, t, FRATURE: NAME/KEY: misc feature OCATION: (51786)..(51786) YTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (51602) .(51602) YTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (102696)...(102696) OTHER INFORMATION: n equals a, FEATURE: NAME/KEY: misc\_feature LOCATTON: (44416) ..(44416) OTHER INPORMATION: n equals a, FEATURE: PEATURE: NAME/KEY: misc feature LOCATION: (107248)..(107248) 'EATURE:

NAME/KEY: misc\_feature LOCATION: (139910)..(139910) OTHER INFORMATION: n equals a, t, g or c NAME/KEY: misc feature LOCATION: {152500}..(152500) OTHER INFORMATION: n equals a, t, g or c FEATURE:
NAME/KEY: misc\_feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t, g or c OTHER INFORMATION: n equals a, t, g or c FEATURE:
NAME/KSY: misc feature
LOCATION: (122167)
OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: [147]97)..(147197) OTHER INFORMATION: n equals a, t, g or FRATURE:
NAME/KEY: misc\_feature
LOCATION: (117136)...(117136)
OTHER INFORMATION: n equals a, t, g or
FRATURE: NAMB/KEY: misc feature LOCATION: (119924)..(119924) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (120038)..(120038) OTHER INFORMATION: n equals a, t, g or FEATURE:
NAME/KEY: misc\_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc\_feature LOCATION: {150841}..(150841) OTHER INFORMATION: n equals a, t, g or NAME/KEY: misc feature LOCATION: (131340) ..(131340) OTHER INFORMATION: n equals a, t, g NAME/KEY: misc feature LOCATION: {121344}..(121344) OTHER INFORMATION: n equals a, t, g FEATURE:
NAME/KEY: misc\_feature
LOCATION: (131360). (131360)
OTHER INFORMATION: n equals a, t, g FEATURE:
NAME/KEY: misc\_feature
LOCATION: (140398). (140398)
OTHER INFORMATION: n equals a, t, 9 NAME, KEY: NAME, KEY: MICATION: (145171)..(145171) OTHER INFORMATION: n equals a, t, g NAME/KEY: misc feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals a, t, FEATURE:
NAME/KEX: misc feature
LOCATION: (145942). (145942)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (142750)..(142750) OTHER INFORMATION: n equals a, PEATURE:

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NAME/KEY: misc_feature
LOCATION: (44965)..(44905)
OTHER INFORMATION: n equals a, t, g or c
FRATURE:
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (51805)...(51805)
OTHER INFORMATION: n equals a, t, g or
FRATURE:
NAME/KEY: misc_feature:
NAME/KEY: misc_feature:
OCATION: (55369)...(55369)
OTHER INFORMATION: n equals a, t, g or
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LOCATION: (51602)...(51602)
OTHER INFORMATION: n equals a, t, g or
FRATURE:
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NAME/KEY: misc_feature
LOCATION: (80024). (80024)
OTHER INFORMATION: n equals a, t, g ox
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LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals a, t, g or
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NAME/KRY: misc_feature
LACATION: (117136). (117136)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a, t, g
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NAME/KRS: misc_feature
LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,
FEATURE:
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LOCATION: (65309) ..(65309)
OTHER INFORMATION: n equals a,
                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a,
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,
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LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (102596)..(102696)
OTHER INFORMATION: n equals a,
                                                                                      NAME/KEY: misc feature
LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a,
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LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals
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                                                                                                                                  0; Gaps
                                                                                      Query Match

84.8%; Score 17.8; DB 15; Length 1830121;
Best Local Similarity 90.5%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAMEKEY: misc feature
LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals a, t, g or C
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9521)...(921)
OTHER INFORMATION: n equals a, t, g or C
FEATURE:
NAME/KEY: misc feature
LOCATION: (10150)...(10150)
COCATION: (10150)...(10150)
FEATURE:
FEATURE:
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LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a, t, g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                t, g or c
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                 1238891 TAACCAAAAACGCATATTGTT 1238911
                                                                                                                                                                          1 TAACCAAAAAGGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals a,
FEATURE:
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a,
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a,
                FEATURE:
NAME/KEY: misc_feature
LOCATION: (152530)..(152530)
                                                                                                                                                                                                                                                                        RESULT 6
US-10-329-670-1
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US-10-424-599-90942/c
; Sequence 90842, Application US/10424599
; Publication No. US20040031072Al
; Sequence 90842, Application US/20440031072Al
; General Information No. US20040031072Al
; APPLICANT: Ea Rosa Thomas J
APPLICANT: Ea Rosa Thomas J
APPLICANT: Cao Yongwei
; TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; TENGTH: 505
; TENGTH: 505
; TYPE: DNA
; ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query March 82.9%; Score 17.4; DB 16; Best Local Similarity 94.7%; Pred. No. 5.2e+02; Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                         US-11-U34-749-749-045

Sequence 6.2. Application US/10094749

Publication No. US20030219741A1

GENERAL INFORMATION:
APPLICANT: SUGIYAMA, TOMOVASU
APPLICANT: SUGIYAMA, TOMOVASU
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, KIRICANDI
APPLICANT: SATO, KIRICANDI
APPLICANT: TONON, YUUKO
APPLICANT: NAGAN, KACRU
APPLICANT: NAGAN, KALICHI
APPLICANT: NAGAN, KALICHI
APPLICANT: NAGAN, KALICHI
APPLICANT: NAGAN, KALICHI
APPLICANT: NAGHNAN, KANULIKO
APPLICANT: NAGANARI, KENUL
APPLICANT: NAGANARI, KENUL
APPLICANT: NAGANARI, KENUL
APPLICANT: PANGHON WUMBER: US/LO/094, 749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 06/350, 435
PRIOR APPLICATION NUMBER: 07 201-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2002-01-1
SEQ ID NO 622
LENGTHARE: PALENTIN VEY: 2.1
SEQ ID NO 622
LENGTHARE: PALENTIN VEY: 2.1
SEQ ID NO 622
LENGTHARE: PALENTIN VEY: 2.1
                                                  1238891 TAACCAAAAACGCATATTGTT 1238911
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               1 TAACCAAAAACGCATATGATT 21
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COCCANISM: Homo sapiens
US-10-094-749-622
                                                                                                                                       RESULT 7
US-10-094-749-622
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84.8%; Score 17.8; DB 16; Length 1830121;
Best Local Similarity 90.5%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, g or
FRATURE:
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals a, t, g or
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NAME/KEY: misc feature
LOCATION: (152500). (152500)

OTHER INFORMATION: n equals a, t, g or FRATURE:
FRATURE:
LOCATION: (152530). (152530)
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LOCATION: (131360)..(131360)
DTHER INFORMATION: n equals a, t, g or
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NAME/KEY: misc feature
LOCATION: (121344)
OTHER INFORMATION: n equals a, t, g
FEATURE:
NAME/KEY: misc feature
LOCATION: (122167). (122167)
OTHER INFORMATION: n equals a, t, g
FEATURE:
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                               Ω
LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a, t,
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a,
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CCATION: (131340)..(131340)
THER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (139910)..(139910)
OTHER INPORMATION: n equals a,
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NAME/KEY: misc_feature
NACATION: (150841)..(150841)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc feature
LOCATION: (145171). (145171)
OTHER INFORMATION: n equals a,
                                                                    NAME/KEY: misc feature
LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals a,
                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: {120038}...(120038)
OTHER INFORMATION: n equals a,
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des M
FILE REFERENCE: BO1/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                           US-10-672-787-41

| Sequence 41, Application US/10672787
| Sequence 41, Application US/10672787
| Sequence 41, Application US/106754A1
| GENERAL INFORMATION:
| APPLICANT: PATTERSON, Chandra
| APPLICANT: PATTERSON, Chandra
| APPLICANT: BERG, Kim, L.
| TITLE OF INVENTION: NUCLECTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
| TITLE OF INVENTION: NUMBER: US/10/672,787
| CURRENT FILING DATE: 2003-09-26
| PRIOR PILING DATE: 2000-06-16
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: PERL Program
| SOFTWARE: PERL Program
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                                                       Gaps
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Pred. No. 1.18+03;
0; Mismatches 2; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 269223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE:
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O
             Length 18154;
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                                                         Indels
           Score 16.8; DB 15;
Pred. No. 1.3e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 13;
Pred. No. 1.8e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3080035 AACCTAAAACGCATATTATT 3080016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142064 AGCCAAAACGCATATCATT 142083
                                                                                                                          9240 TAAACAAAACGCATATAAT 9221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10312841 Publication No. US20030186277A1 GENERAL INFORMATION:
                                                                                                   1 TAACCAAAACGCATATGAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AACCAAAAACGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Moraxella catarrhalis
US-10-672-787-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AACCAAAAACGCATATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.03
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
, LOCATION: (379615)
US-10-312-841-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-312-841-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Sequence 228, Application US/10311455
Publication Wo. US20030143606A1
GENERAL INFORMATION:
APPLICANT: DIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: With With Christian
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 228
LENGTH: 18154
                                                                                                                                                                                                                                                                           RESULT 9

US-10-369-493-34760

i Sequence 34760, Application US/10369493

j Publication No. US20030233675A1

general invormation:
   APPLICANT: Cao, Yongwei

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PRAPESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PRAPESSION OF MICROBIAL PROFEINS

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT PILING DATE: 2003-02-28

PRIOR PILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 34760

LENGTH: 4169
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; FRATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-228
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                                                                                     Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                              Indels
                                                                                Query Match
Best Local Similarity 90.0%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8; DB 16;
Pred. No. 9.9e+02;
0; Mismatches 2;
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53131C.1
US-10-424-599-90942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2074 TAACCAAAACACATATGCT 2093
                                                                                                                                                                                                                 319 AACCAAACACGCATATGTTT 300
                                                                                                                                                                          2 AACCAAAACGCATATGATT 21
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US-10-369-493-34760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-10-311-455-228/c
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us-10-676-299-8.rnpb

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US-09-867-701-10855/c
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J
APPLICANT: APPLICANT: Alou Yikua
APPLICANT: Chou Yikua
APPLICANT: Co Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Emprovement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Emprovement
CURRENT APPLICANT: 2003-04-28
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.1%; Score 16.4; DB 13; Length 33805; Best Local Similarity 94.4%; Pred. No. 2.18+03; Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 77.1%; Score 16.2; DB 13; Length 177; Best Local Similarity 85.7%; Pred. No. 1.1e+03; Matches 18; Conservative 0; Mismatches 3; Indels 0;
                                                                                     APPLICANT: MORTIS, David W.
APPLICANT: Engelhard, Eric K.
TITLE OP INVENTION: ADDED
TITLE OP INVENTION: ADDED
TITLE OP INVENTION: ADDED
TITLE OP INVENTION: CANGER
FILE REFERENCE: 52945200012
CURRENY PILLING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 99/747,377
PRIOR PILLING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_70483C.1 US-10-424-599-110156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (1)...(177)
OTHER INFORMATION: unsure at all n locations
                      Sequence 1483, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAACCAAAACGCATATGATT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(33805)
/ OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            653 TAACCAAAAACTCATATG 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TAACCAAAAACGCATATG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-10-424-599-110156/c
US-10-087-192-1483
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RESULT 15

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0; Gaps
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Sequence 10855, Application US/09867701
Patent No. US2002013237A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ 1D NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
EXRO ID NO 10855
LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TAACCAAAACGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 TAACTAAAAGGCATCTGATT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7%
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
GRGANISM: Homo sapien
US-09-867-701-10855
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Search completed: May 27, 2004, 06:17:00 Job time : 453.128 secs

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May 26, 2004, 17:50:29; Search time 513.248 Seconds (without alignments) 221.574 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3: /cgn2 6/ptodata/2/pubpna/USO6 NEW PUB.seq:*
4: /cgn2 6/ptodata/2/pubpna/USO6 PUBCOMB.seq:*
5: /cgn2 6/ptodata/2/pubpna/USO6 PUBCOMB.seq:*
6: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
7: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
8: /cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
10: /cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
10: /cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
11: /cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
12: /cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
13: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
14: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
15: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
16: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
17: /cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
16: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
17: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
18: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
19: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
19: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
19: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5920802
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2960401 seqs, 2274450654 residues
                                                                                                                                                                                                                                                                                                                                                                                                                      1 ttaagtcatatatgtttttgactta 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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25
                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 9, Appli	Sequence 10, Appl	Sequence 6, Appli	Sequence 5, Appli	Seguence 3339, Ap	Seguence 197612,	Seguence 197612,	Seguence 3647, Ap	Seguence 3647, Ap	Sequence 1370, Ap	Sequence 135777,	Sequence 2768, Ap	Seguence 206167,	Sequence 206167,	
ΩI	US-10-222-952A-9	. US-10-222-952A-10	US-10-222-952A-6	US-10-222-952A-5	US-10-282-122A-3339	US-10-027-632-197612	US-10-027-632-197612	US-09-938-842A-3647	US-09-938-842A-3647	US-10-311-455-1370	US-10-424-599-135777	US-09-783-590-2768	US-10-027-632-206167	US-10-027-632-206167	
DB	15	15	15	15	13	ř	9	σ	11	15	13	σ	13	16	
Query Match Length DB	25	25	40	42	401	650	650	2000	2000	5641	798	283	537	537	
Query Match	100.0	100.0	100.0	100.0	100.0	83.2	83.2	80.8	80.8	80.8	79.2	76.8	76.8	76.8	
Score	25	25	25	25	25	20.8	20.8	20.2	20.2	20.2	19.8	19.2	19.2	19.2	
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Result No.	•	Ų	U		Ų	U	υ	U	υ		Ú	Ü	U	Ų	

Sequence 106547,	Sequence 1, Appli		Sequence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence 15	Sequence 86, Appl	2097	12		Sequence 438, App	Sequence 56865, A			Sequence 7, Appli		Sequence 5870, Ap	Sequence 1900, Ap	1108,		Sequence 164169,	16416	22	m	₹	Ä	Sequence 2058, Ap
US-10-424-599-106547	US-09-790-988-1	US-10-424-599-83711	US-10-424-599-80042	US-10-027-632-262525	US-10-027-632-262525	US-10-424-599-126150	US-10-369-493-46160	US-10-424-599-49551	US-10-311-455-1564	US-10-240-589C-86	US-10-311-455-2097	US-10-240-589C-127	US-10-087-192-2014	US-10-311-455-438	US-10-424-599-56865	US-10-115-123-73	US-10-012-542-73	US-10-006-852-7	US-10-204-708-1	US-09-764-891-5870	US-10-087-192-1900	US-10-087-192-1108	US-10-292-798-1095	US-10-027-632-164169	US-10-027-632-164169	US-10-425-114-2142	US-10-081-327-37	US-10-081-327-44	5 US-10-398-221-10	S US-10-398-221-2058
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1494	640681	344	366	2274	2274			2753	_	10279		73334	N					2121	_			118931	358246		718	N	ä	193303	1163020	3011208
76.8	75.2	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	73.6	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	71.2	71.2	71.2	71.2	71.2	71.2	71.2
19.2	18.8	18.6	18.6	18.6	18.6	18.6	ú				18.6											18.2		60		17.8		17.8	17.8	17.8
15	16	17	18	19	20	21	22	23	24	25	56	27	28	5	30	1	32	8	4	S	36	37	38	6	40	41	42	43	44	45
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## ALIGNMENTS

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TYPE: DNA ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence FRATURE: OTHER INFORMATION: CHROMASIT top, short biotinylated oligo sequence; biotinylated OTHER INFORMATION: nucleotide at position 1
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   Sequence 9, Application US/1022952A
; Bequence 9, Application US/1022952A
; Publication No. US20030096275A1
; GENERAL INFORMATION:
    APPLICANT: Regenesis
; APPLICANT: Laing, Lance
; TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
; FILER REFERENCE: 4107/1L/43.US1
; CURRENT APPLICATION NUMBER: US/10/222,952A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/313,714
; PRIOR FILITED DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 13
; SOFTHARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 25; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels
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US-10-222-952A-9
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RESULT 2 US-10-222-952A-10/c Sequence 10, Application US/10222952A Publication No. US20030096275A1

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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 42
                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-10-282-122A-3339/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/1022952A
Sequence 6, Application US/1022952A
GENERAL INFORMATION:
APPLICANT: Regensis
APPLICANT: Laing, Lance
ITILE NO INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REPERRACE: 4107/11443-US1
CURRENT FILING DATE: 2002-08-15
PRIOR PILICATION NUMBER: US 60/313,714
PRIOR PLUICATION NUMBER: US 60/313,714
PRIOR PLUICATION NUMBER: 13 60/313,714
SROR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 15; Length 25; 100.0%; Pred. No. 2.2; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 15; Length 40; 100.0%; Pred. No. 2.4; tive 0; Mismatches 0; Indels
                    APPLICANT: REGENESSIS
APPLICANT: REGENESSIS
APPLICANT: Laing, Lance
TITLE OF INVENTION: BIGSENSOR FOR SMALL MOLECULE ANALYTES
FILE REFERENCE: 4107/11443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT PILING DATS: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Regenesis
APPLICANT: Regenesis
APPLICANT: Laing, Lance
TITLE OF INVENTION BIGSENSOR FOR SMALL MOLECULE ANALYTES
FILE REPRENCE: 4107/11443-US1
CURRENT APPLICATION NUMBER: US/10/22,952A
CURRENT APPLICATION NUMBER: US/60/20313,714
PRIOR APPLICATION NUMBER: US 60/313,714
                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: CHROMSIB bottom short oligo sequence US-10-222-952A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: CHROMLIB bottom, long oligo sequence US-10-222-952A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TIAAGICATATATGTTTTGACTTA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-10-222-952A-5
IS-10-222-952A-5

* Sequence 5, Application US/1022952A

* Publication No. US20030096275A1

* GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       TYPE DNA
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.09
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-222-952A-6/c
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) OTHER INFORMATION: CHROMLIT top, long biotinylated oligo sequence, biotinylated , OTHER INFORMATION: nucleotide at position 1 US-10-222-952A-5
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITAR.024

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/291,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLICATION NUMBER: 60/230,335

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-03-09

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Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                              Length 42;
                                                                                                                                                                                                                                                                                                                     Indele
                                                                                                                                                                                                              Query Match
100.0%; Score 25, DB 15,
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 25, Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3339, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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us-10-676-299-9.rnpb

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Query Match 80.8%;
Best Local Similarity 88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .09-938-842A-3647/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-938-842A-3647/c
                                                                                                                                                                                                 US-10-027-632-197612
                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-938-842A-3647
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                                                                                                                                                                                                                                                             Sequence 197612, Application US/10027632
| Publication No. US20020198371A1
| GENERAL INFORMATION: US20020198371A1
| GENERAL INFORMATION: US20020198371A1
| GENERAL INFORMATION: US20020198371A1
| GENERAL INFORMATION: US4016 G.
| TITLE OF INVENTION: US4016 G.
| FILE REFERENCE: 108827.129
| CURRENT FILING DATE: 2002-04-30
| PRIOR APPLICATION NUMBER: US 60/198,676
| PRIOR PILING DATE: 2000-07-12
| PRIOR PILING DATE: 2000-03-29
| PRIOR PILING DATE: 2000-03-29
| PRIOR PLING DATE: 1099-11-23
| PRIOR PILING DATE: 1099-11-23
| PRIOR PILING DATE: 1999-11-23
| PRIOR PILING DATE: 1999-11-23
| PRIOR PILING DATE: 1999-11-23
| PRIOR PILING DATE: 1999-10-28
| PRIOR PILING DATE: 1999-10-28
| PRIOR PILING DATE: 1999-10-38
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TILE REFERENCE: 108927.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2000-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1099-108

PRIOR PILING DATE: 1099-108

PRIOR PILING DATE: 1099-108

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-09-8
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83.2%; Score 20.8; D
Best Local Similarity 91.7%; Pred. No. 1.6e
Matches 22; Conservative 0; Mismatches
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US-US-JS-SEAGA-JS-JK/C

Sequence 3647, Application US/09938842A
Fatent No. US20020160378A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harper, Joef
APPLICANT: Kreps, Joef
APPLICANT: WANG, Xun
APPLICANT: WANG, Xun
APPLICANT: APPLICANT: Out
APPLICANT: WANG, Xun
APPLICANT: Out
APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/224,865
FILE REFERENCE: SCRIP1300-3
FRIOR APPLICATION NUMBER: US 60/264,647
FRIOR PELING DATE: 2001-08-24
FRIOR PILING DATE: 2001-01-16
FRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
INTER OF SEQ ID NOS: 5379
INTOR THE DNA
TYPE: DNA
TYPE: DNA
APPLICATION NUMBER: US 60/300,111
FRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
ILENGTH: 2000
TYPE: DNA
APPLICATION ADMINISTRY
APPLICATION NUMBER: US 60/300,111
FRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
TYPE: DNA
APPLICATION ADMINISTRY
APPLICATION NUMBER: US 60/300,111
FURNATH: 2000
TYPE: DNA
APPLICATION ADMINISTRY
APPLICATION ADMINISTRY
APPLICATION NUMBER: US 60/300,111
FURNATH: 2000
TYPE: DNA
APPLICATION ADMINISTRY
APPLIC
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Publication No. US20040069476A9

GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Mang, Xun
APPLICANT: Wang, Xun
APPLICANT: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
ITILE OF INVENTION: STRESS: US/09/938, 842A
ITILE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR APPLICATION NUMBER: US 60/227, 866

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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Pred. No. 3.2e+02;
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 197612
LENGTH: 650
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Sequence 276, Application US/09783590

Patent No. US20020110850A1

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Handong
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICANT: E100-16.2C1
CURRENT APPLICANTON: NUMBER: US/09/783,590
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
FILE REPERENCE: PO-16.2C1
CURRENT FILING DATE: 1995-04-12
FRIOR FILING DATE: 1994-11-21
SPRIOR FILING DATE: 1994-11-21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2768
LENGTH: 283
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US-10-027-632-206167/. Application US/10027632
Sequence 206167, Application US/10027632
Publication No. US2020198371A1
STEMERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.12
CURRENT APPLICATION NUMBER: US/10/027,632
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                                                                                        Length 798;
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                                                                                                                                          Indels
                                                                                  Score 19.8; DB 13;
Pred. No. 4e+02;
0; Mismatches 2;
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93615C.1
US-10-424-599-135777
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OTHER INFORMATION: n equals a,t,g, or c
NAMB/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,9, or on NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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                                                                                  Query Match 79.2%;
Best Local Similarity 91.3%;
Matches 21; Conservative (
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc feature
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Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: DIEPENBROCK, Christian

APPLICANT: DEEK, Mignesis of Diseases Associated with the Immune System by Determ

ITILE OF INVENTION: Cytosine methylation

FILLE REPERENCE: 5013.104

FILLE REPERENCE: 5013.104

FILLE REPERENCE: 5013.104

FILLS REPERENCE: 5013.104

FRICH RAPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2000-107-02

PRIOR PILING DATE: 2000-06-30

FRICH PRIOR PILING DATE: 2000-06-30

FRICH PRIOR PILING DATE: 2000-09-01

FRICH PILING DATE: 2000-09-01
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomes J
APPLICANT: La Rosa Thomes J
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 135777
LENGTH: 798
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, OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1370
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Best Local Similarity 88.0%; Pred. No. 3.8e+02;
Matches 22; Conservative 0; Mismatches 3;
                                                                                                                                                                                            Query Match 80.8%; Score 20.2; DB 11;
Best Local Similarity 88.0%; Pred. No. 3.2e+02;
Matches 22; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                         1 TTAAGTCATATATGTTTTTGACTTA 25
                                                                                  ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3647
LENGTH: 2000
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ORGANISM: Glycine max
FEATURE:
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US-10-311-455-1370
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Search completed: May 27, 2004, 06:17:06 Job time : 519.248 secs
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Sequence 20667, Application US/10027632

Publication No. US20030204075A9

SEGNERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERENCE: 108827.129

CURRENT APPLICATION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129

CURRENT PILING DATE: 2002-04-30

PRIOR PILING DATE: 2000-04-10

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1000-02-24

PRIOR PILING DATE: 1000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/166,002

PRIOR APPLICATION NUMBER: US 60/166,002

PRIOR PILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FRANCE PRIOR NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09
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            PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 1900-02-24
PRIOR PLING DATE: 1999-11-23
PRIOR PILING DATE: 1999-04-26
PRIOR PILING DATE: 1999-09-26
PRIOR PILING DATE: 1999-09-3
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| NAME/KEY: misc feature
| LOCATION: (1)...(537)
| OTHER INFORMATION: n = A,T,C or G
| US-10-027-632-206167
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| DOCATION: (1)...(537)
| CTHER INFORMATION: n = A,T,C or G
US-10-027-632-206167
2002-04-30
CURRENT FILING DATE:
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US-10-027-632-206167/c
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US-10-44-599-106547/c

Sequence 106547, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Aco Younge i
APPLICANT: Coo Younge i
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 19-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
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Query Match 76.8%; Score 19.2; DB 16; Length 537; Best Local Similarity 87.5%; Pred. No. 6.4e+02; Matches 21; Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: PAT_MRT3847_67228C.1
US-10-424-599-106547
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Sequence 9, Appli
Sequence 10, Appli
Sequence 5, Appli
Sequence 3339, Ap
Sequence 197612,
Sequence 197612,
Sequence 197612,
Sequence 3847, Ap
Sequence 1377,
Sequence 2768, Ap
Sequence 2768, Ap
                                                                         May 26, 2004, 17:50:29; Search time 513.248 Seconds (without alignments) 221.574 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-222-952A-10

5 US-10-222-952A-5

3 US-10-222-952A-5

3 US-10-222-952A-5

6 US-10-282-127612

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0 US-09-938-842A-3647

1 US-09-938-952-1370

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US-10-027-632-206167
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Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match
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Perfect score:
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1494 40681 3464 2274 2274 2274 2753 10279 73334 248436	10891 1486 1486 1486 10872 10872 10872 10872 10873 118931 1183303 1193303 3011208	SULT 1 -10-222-952A-9/C -10-222-952A-9/C -10-222-952A-9/C -10-222-952A-9/C -10-222-952A-9/C -10-222-952A-9/C -10-222-952A-9/C -10-222-952A-9/C -10-222-952A-9/C -10-222-952A-10-22-952A-10-22-9-2-9-2-9-2-9-2-9-2-9-2-9-2-9-2-9-2	
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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels

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RESULT 2 US-10-222-952A-10 Sequence 10, Application US/10222952A ; Publication No. US20030096275Al

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TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

CTHER INFORMATION: CHROMLIT top, long biotinylated oligo sequence; biotinylated

US-10-222-952A-5
                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 25; DB 15; Length 42; Best Local Similarity 100.0%; Pred. No. 2.4; Matches 25; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 25; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
NUMBER OF SEQ ID NOS: 13
SOFWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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100.0%; Score 25; DB 15; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10222952A

Publication No. US2030096275A1

GENERAL INFORMATION:
APPLICANT REGENESS:
APPLICANT LAING, LANGE SON SMALL MOLECULE ANALYTES
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10222952A
Sequence 5, Application US/10222952A
Publication No. US20030096275A1
SERERAL INFORMATION:
APPLICANT: Regenesis
APPLICANT: Laing, Lance
TITLE OF INVENTION: BIOGENSOR FOR SMALL MOLECULE ANALYTES
FILE REFERENCE: 4107/1L443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
                                                      APPLICANT: Laing, Lance
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REFERENCE: 4107/11443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR APPLICATION NUMBER: US 60/313,714
SRIOR PILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 10
LENGTH: 25
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; OTHER INFORMATION: CHROMLIB bottom, long oligo sequence US-10-222-952A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: CHROMSIB bottom short oligo sequence US-10-222-952A-10
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                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
        GENERAL INFORMATION:
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LENGTH: 40
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                             DB 13; Length 401;
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 197612
LENGTH: 650
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                 : TYPE: DNA
: ORGANISM: Human
US-10-027-632-197612
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US-09-938-842A-3647
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                                                                                                                                                                                                                                                                                                       Matches
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; Sequence 197612, Application US/10027632
; Publication No. US20030204075A9
; GeneraAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Mucleotide
TITLE OF INVENTION: Identification and Mapping of Single Mucleotide
FILE OF INVENTION: Identification and Mapping of Single Mucleotide
FILE OF INVENTION: Identification and Mapping of Single Mucleotide
FILE OF INVENTION: Identification and Mapping of Single Mucleotide
FILE OF INVENTION: 108027.12
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR APPLICATION NUMBER: US 60/165,383
; PRIOR PLING DATE: 1099-11-23
; PRIOR FILING DATE: 1099-11-23
; PRIOR FILING DATE: 1099-11-23
; PRIOR FILING DATE: 1099-10-28
; PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                     Sequence 197612, Application US/10027632

Sequence 197612, Application US/10027632

Publication No. USS02020198371A1

GENERAL INPORMATION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: USANDERS: US/10/027,632

CURRENT FILING DATE: 2000-04-30

FRICH REPRINGE DATE: 2000-07-12

FRICH REPLIANG DATE: 2000-07-12

FRICH APPLICATION NUMBER: US 60/198,676

FRICH APPLICATION NUMBER: US 60/193,483

FRICH APPLICATION NUMBER: US 60/193,483

FRICH RILING DATE: 2000-03-29

FRICH RELING DATE: 2000-03-29

FRICH RELING DATE: 2000-03-29

FRICH APPLICATION NUMBER: US 60/165,318

FRICH APPLICATION NUMBER: US 60/165,358

FRICH APPLICATION NUMBER: US 60/166,358

FRICH APPLICATION NUMBER: US 60/166,358

FRICH APPLICATION NUMBER: US 60/166,358

FRICH APPLICATION NUMBER: US 60/166,002

FRICH APPLICATION NUMBER: US 60/166,002
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                                                                       1 TAAGTCAAAACATATATGACTTAA 25
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CRGANISM: Human
US-10-027-632-197612
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US-10-027-632-197612
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Sequence 342A, Application US/09938842A

Facent No. US2020160378A1

Facent No. US2020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: AND WETHODS OF USE

TITLE OF INVENTION: SAME, AND WETHODS OF USE

FILE REFERENCE: 2001-08-24

CURRENT PILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR PLING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 3647

FILENCENT: 2000

WADDER OF SEQ ID NOS: 5379
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Publication No. US20040009476A9

Publication No. US20040009476A9

GENERAL INFORMATION:

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: AND TONG

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR PILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR PLING DATE: 2001-01-16

PRIOR PELING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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ch 83.2%; Score 20.8; DB 16; Length 650; 1 Similarity 91.7%; Pred. No. 1.66+02; 22; Conservative 0; Mismatches 2: Indels A.
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80.8%; Score 20.2; DB 9; Length 2000;

Best Local Similarity 88.0%; Pred. No. 3.2e+02;

Matches 22; Conservative 0; Mismatches 3; Indels 0
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Sequence 2768, Application US/09783590

Sequence 2768, Application US/09783590

Sequence 2768, Application US/09783590

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Haadong
APPLICANT: Li, Haadong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
CURRAT APPLICATION NUMBER: US/09/783, S90
CURRAT FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485

SOFTWARE: Patentin Ver. 2.0

SRQ ID NO 2768
LENTILL: 283
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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                                                                       Length 798;
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76.8%; Score 19.2; DB 9; Length 283;
Best Local Similarity 84.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 4; Indels (
                                                                                                                    Indels
                                                                     Query Match
79.2%; Score 19.8; DB 13;
Best Local Similarity 91.3%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 2;
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93615C.1
US-10-424-599-135777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (140)
UDCATION: (140)
UDCATION: (170)
UDCATION: (179)
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UDCATION: (179)
UDCATION: (205)
UDCATION: (205)
UDCATION: (205)
UDCATION: (206)
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COTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-2768
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                                                                                                                                                                   2 AAGTCAAAACATATATGACTTA 24
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FEATURE:
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US-10-027-632-206167
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Sequence 1370, Application US/10311455

Publication No. US20030143606A1

SEQUENCE 1370, Application No. US20030143606A1

APPLICANT: DIBK, Alexander

APPLICANT: PIRPERBROCK, Christian

APPLICANT: DIBKLIM, Kurt

ITILE OF INVENTION: Oylosine methylation

TITLE OF INVENTION: Oylosine methylation

TITLE OF INVENTION: Oylosine methylation

TITLE OF INVENTION: Oylosine methylation

FILE REPERBRES: 5013.4014

CURRENT APPLICATION NUMBER: DC7/EP01/07377

PRIOR FILING DATE: 2001-07-02

PRIOR PILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

SEQ ID NO 1370

SEQ ID NO 1370

SEQ ID NO 1370

SEQ ID NO 1370
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vongwei
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE SPERENT APPLICATION NUMBER: US/10/424,599
CURRENT APLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 135777
LENGTH: 798
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1370
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                                                                                                                                                                        Length 2000;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                      Query Match 80.8%; Score 20.2; DB 11; Best Local Similarity 88.0%; Pred. No. 3.2e+02; Matches 22; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1536 TAATTCAAAAAATATATATAACTTAA 1512
                                                                                                                                                                                                                                                                                             1 TAAGTCAAAACATATATGACTTAA 25
                                                                                                                                                                                                                                                                      1 TAAGTCAAAACATATATGACTTAA 25
                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.0
Matches 22; Conservative
            NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3647
LENGTH: 2000
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ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-424-599-135777
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US-10-311-455-1370/c
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Squence 106547, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TTILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TTILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 106547
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     Query Match 76.8%; Score 19.2; DB 16; Length 537; Best Local Similarity 87.5%; Pred. No. 6.4e+02; Matches 21; Conservative 0; Mismatches 3; Indels 0;
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US-10-424-599-106547
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US-10-027-632-206167
Sequence 206167, Application US/10027632
Sequence 206167, Application Wo. US20030204075A9
Sequence 206167, Application Wo. US20030204075A9
SEMERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPRENCE: 108027, 129
CURRENT FILING DATE: 2002-04-30
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PELING DATE: 12000-02-28
PRIOR PELING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/165,358
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-08
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PR
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NAME/KEY: misc_feature

LOCATION: [1]...[537)

CTHER INFORMATION: n = A,T,C or G
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Search completed: May 27, 2004, 06:17:09 Job time: 516.248 secs

NAME/KEY: misc\_feature | DOCATION: (1)...(537) | OTHER INFORMATION: n = A,T,C or G US-10-027-612-206167

ORGANISM: Human

SEQ ID NO 206167

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                                                                                                             May 26, 2004, 16:18:00; Search time 33.4745 Seconds (without alignments) 348.146 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                        682709 segs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                 US-10-676-299-8
21
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Sequence 1995, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC-007
GURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 475, App
Sequence 475, App
Sequence 175, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 102, Appli
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US-09-557-884-1
j Sequence 1, Application US/09557884
j Patent No. 6506581
j GENERAL INFORMATION:
j TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
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CORRESSPONDENCE ADDRESS:
ADDRESSEE Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
4 US-09-718-841-1

4 US-09-718-810-1

4 US-09-311-626B-5

4 US-09-431-475-6

4 US-09-48-513-475-6

4 US-09-685-166A-475-7

4 US-08-148-81D-1

4 US-08-148-81D-1

4 US-08-148-90-2

4 US-09-581-909-2

4 US-09-581-909-2

4 US-09-581-909-2

4 US-09-581-381-1

4 US-08-916-421B-1

4 US-08-916-421B-1

4 US-08-916-421B-1

4 US-08-916-421B-1

4 US-08-916-421B-1

6 US-08-916-421B-1

7 US-08-916-421B-1

8 US-08-918-461-5

9 US-09-328-111-408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; Ctaphylococcus epidermidis US-09-134-001C-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 TAACTAAAAAGCATATGATT 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TAACCAAAACGCATATGATT 21
 Query Match
Best Local Similarity
---- 19; Conserve
                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-134-001C-1995
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J. Craig Venter
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1830121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
CPREATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: AUMINOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

84.8%; Score 17.8; I

Best Local Similarity 90.5%; Pred. No. 20;

Matches 19; Conservative 0; Mismatches
CCMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCI Text
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFFICATION: UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
FILING DATE: 1995-04-21
ATTORNEY/AGET INDOMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1238891 TAACCAAAAACGCATATTGTT 1238911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                            TELEPHONE: 301-309-8504
TELEPAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TAACCAAAAACGCATATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville,
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-643-990A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-557-884-1
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US-09-543-681A-815

US-09-543-681A-815

Sequence 815, Application US/09543681A

Sequence 816, Application US/09543681A

Sequence 817, Application US/09543681A

Sequence 818, Application US/09543681A

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US/09/543, 681A

CURRENT APPLICATION NUMBER: US/09/543, 681A

CURRENT FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER: OF SEQ ID NOS: 8344

SEQ ID NO 815

LENGTH: 678
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APPLICANT: Betg. Kim, L.
APPLICANT: Betg. Kim, L.
TITLE OP INVENTION: UNCLEOTIDE SEQUENCES OP MORAXELLA CATARRHALIS GENOME
TITLE OP INVENTION: WULLEOTIDE SEQUENCES OP MORAXELLA CATARRHALIS GENOME
TILL REPERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596, DO2
CURRENT FILING DATE: 1999-06-16
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOPTWARE: PERL Program
SEQ ID NO 41
LENGTH: 269223
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                                                                                                                                                                                                                                                                                                         DB 4; Length 1830121;
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ORGANISM: Moraxella catarrhalis

STATURE: ASTATURE:

O'THER INFORMATION: Incyte template ID No. 6632636 41

US-09-596-002-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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80.0%; Score 16.8; D

Best Local Similarity 90.0%; Pred. No. 50;

Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                       Query Match 84.8%; Score 17.8; I Best Local Similarity 90.5%; Pred. No. 20; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1238891 TAACCAAAAACGCATATTGTT 1238911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142064 AGCCAAAACGCATATCATT 142083
                                                                    INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 41, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                            1 TAACCAAAAACGCATATGATT 21
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                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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Sequence 9, Application US/09071296
Patent No. 6177245
GENERAL INFORMATION:
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NX
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
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US-08-472-028A-9/C
US-08-472-028A-9/C
Sequence 9, Application US/08472028A
Patent No. 5767373
GENERAL INFORMATION:
APPLICANT: Ward, Exic R
APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Bukaryotic Organisms
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.1%; Score 16.2; DB 1; Length 1697;
85.7%; Pred. No. 59;
                                                                                                                                                           DB 4; Length 678;
                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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LOCATION: 29..1501

CTHER INFORMATION: /note= "Arabidopsis protox-3 cDNA;

OTHER INFORMATION: sequence from pwDC-5"
US-08-472-028A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,028A
FILING DATE:
CLASSIFICATION: BOOT
APPLICATION NUMBER: 36,129
REPERENCE/DOCKET NUMBER: 36,129
REPRENCE/DOCKET NUM
                                                                                                                                                       Score 16.4; D
Pred. No. 43;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1667 TAAGCTAAAAGGCATATGATT 1647
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                                                                                                                                                                                                                                                                                                           4 CCAAAAACGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                   47 CCAAAAAGCATATGATT 64
                                                                                                                                                   Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
; TYPE: DNA; ORGANISM: Proteus mirabilis US-09-543-681A-815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10532
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GENERAL INFORMATION:
APPLICANT: Ward, Bric R
APPLICANT: Wolath, Sandra
APPLICANT: Condage Enzyme Activity in Bukaryotic Organisms
TITLE OF INVENTION: Oxidage Enzyme Activity in Bukaryotic Organisms
WUNDABR OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
CORRESPONDENCE ADDRESS: 7 Skyline Drive
CITY: Hawthorne
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 1053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Pacentin Release #1.0, Version #1.25
COMPUTER: Pacentin Release #1.0, Version #1.25
COMPUTER: Date: Oc-UN-1995
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,296
FILING DATE: Oc-UN-94
ATTORNEY/AGENT INFORMATION:
RESISTRATION NUMBER: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
RESISTRATION NUMBER: 26,129
REFERENCE/DOCKET NUMBER: CGC 1748/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-196-268-9/c

) Sequence 9, Application US/09196268

) Sequence 9, Application US/09196268

) Sequence 9, Application US/09196268

) GREERAL INFORMATION:

APPLICANT: Ward, Eric R

APPLICANT: Wolzelh, Sandra

) TITLE OF INVENTION: Manipulation of Protoporphyrinogen

TITLE OF INVENTION: Oxidae Enzyme Activity in Eukaryotic Organisms

) WURBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

) CORRESPONDENCE ADDRESS:

) STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GTHER INFORMATION: /note= "Yeast protox-3 cDNA;

OTHER INFORMATION: sequence from pWDC-5"
US-09-071-296-9
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85.7%; Pred. No. 59;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1667 raagcraaaagccarargarr 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNE.

RAME: Blmer, c. R. REGISTRATION NUMBER: 150. - CGC 1
REFERENCE/DOCKET NUMBER: CGC 1
TELECHONICATION INFORMATION:
TELEFRAX: 919-541-8649
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARCTERISTICS:
LENGTH: 1697 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TAACCAAAAACGCATATGATT
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RESULT 7 US-09-071-296-9/c

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ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
LOCATION: 29.1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09015683
Sequence 9, Application US/09015683
Sequence 9, Application US/09015683
Sequence 9, Application US/09015683
Setent No. 628806
CENERAL INFORMATION:
APPLICANT: Ward, Eric R
APPLICANT: Waltath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STREET: NY
COUMTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/015,683
FILING DATE:
FILING DATE:
STREET: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.1%; Score 16.2; DB 3; Length 1697;
85.7%; Pred. No. 59;
tive 0; Mismatches 3; Indels 0;
                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSTAILON NUMBER: US/09/196,268
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REPERENCE/DOCKET NUMBER: GC 1748/CIP
TELECOMMUNICATION INFORMATION:
TELEPRAX: 919-541-8614
TELEPRAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1697 base pairs
TYPE: muclaic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS

COCATION: 29..1501

OTHER INFORMATION: /note= "Yeast protox-3 cDNA;

OTHER INFORMATION: sequence from pWDC-5"
US-09-196-268-9
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-015-683-9/c
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RESULT 10
US-09-191-998-9/C
US-09-191-998-9/C
Sequence 9, Application US/09191998
Sequence 9, Application US/09191998
PATENT Nand Bric R
APPLICANT: Wolrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Claba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1697;
                                                                                                                                                                                                                                                                                                                                                                         , LUCATION: 29..1501
; OTHER INFORMATION: /note= "Arabidopsis protox-3 cDNA;
; OTHER INFORMATION: sequence from pWDC-5"
US-09-015-683-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,998
FILING DATE: 06-JUN-1995
CLASSIPICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATYONEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
RELEFAX: 919-541-8614
TELEFRAX: 919-541-8619
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
77.1%; Score 16.2; DB 3;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 3;
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REPERBRUCE/DOCKET NUMBER: CGC 1748/CIP
TELEPHONE: 919-541-8614
TELEPHONE: 919-541-8614
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1697 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
```

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US-545-3281-7.0

1 Sequence 1, Application US/08545528D

1 Patent No. 653773

2 GENERAL INFORMATION:

3 APPLICANT: Fraser et al.

1 TILE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragmen

2 Patent No. 6537773

3 TILE OF INVENTION: Thereof, and Uses Thereof

FILE REFERENCE: PB193P1

3 CURRENT APPLICATION NUMBER: US/08/545,528D

5 CURRENT PILING DATE: 1995-10-19

6 PRIOR PILING DATE: 1995-06-07

7 PRIOR PILING DATE: 1995-06-07

8 PRIOR PILING DATE: 1995-06-07

8 PRIOR PILING DATE: 1995-06-07

8 PRIOR FILING DATE: 1995-06-07

9 PRIOR FILING DATE: 1995-06-07
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Patent No. 6503729
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: jannaschii
FILLE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
FILLE REFERENCE: PB275
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
RIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
RIOR PERIOR IN NOS: 3
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1.
SEQ ID NO 1.
SEQ ID NO 1.
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                                                                                                                                ö
                                                                       DB 4; Length 7210;
                                                                                                                                3; Indels
                                                                   Query Match 77.1%; Score 16.2; Dest Local Similarity 85.7%; Prest Local Similarity 85.7%; Prest Cheek 18; Conservative 0; Mismatches
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NAMESKEY:
NAMESKEY:
LOCATION: (28222). (28222)
OTHER INFORMATION: n equals a, t, c, or
NAMESKEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or
NAMESKEY: misc feature
LOCATION: (84773)..(84773)
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                                                                                                                                                                                                                                                          4301 TAACCAAATCGCAAATGCTT 4321
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ORGANISM: Methanococcus jannaschii
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-545-528D-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-916-421B-1
      JS-09-634-238-15
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US-09-128-352-3794
US-09-128-352-3794
I Sequence 3194, Application US/09328352
Factor No. 6562958
GENERAL INPORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3794
LENGRENT: 2235
TERMEDIA 2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Glenh, Matthew
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Bloksberg, Leonard, N.
APPLICANT: Bloksberg, Leonard, N.
APPLICANT: Bloksberg, Leonard, N.
APPLICANT: Christensson, Anna C.
APPLICANT: Croole, Paul W.
APPLICANT: Coolbear, Timothy
ITTLE OF INVENTION: Polymodectides, materials incorporating
ITTLE OF INVENTION: them and methods for using them.
FILE REPERENCE: 11000.104301
FILE REPERENCE: 11000.104301
FILE OF INVENTION: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWAREN: FastsEQ for Windows Version 4.0
IENGTH: 7210
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                      Query Match 77.1%; Score 16.2; DB 4; Length 1697; Best Local Similarity 85.7%; Pred. No. 59; Matches 18; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 2235;
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                                                                                                                                                           NAME/KEY: CDS

LOCATION: 29..1501

COTHER INFORMATION: /note= "Yeast protox-3 cDNA;

CTHER INFORMATION: sequence from pWDC-5"

US-09-191-998-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.1%; Score 16.2; C
85.7%; Pred. No. 61;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1667 TAAGCTAAAAGGCATATGATT 1647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-634-238-15
US-09-634-238-15
Sequence 15, Application US/09634238
Patent No. 6544772
GENERAL INFORMATION
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Havukkala, Ilkka J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TAACCAAAAAGGCATATGATT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
) ORGANISM: Acinetobacter baumannii
US-09-328-352-3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Lactobacillus rhamnosus
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Best Local Similarity 85.7
Matches 18; Conservative
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
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TTAMECANT	nisc_feature (84808)(84	KEY: misc featur ION: (84812)(8	INFORMATION: n equals KEY: misc_feature	TON: (98120)(98120) INFORMATION: n equals	Misc realure (98159)(98159) ORMATION: n equals	KEY: misc feature ION: (98239).,(98239)	INFORMATION: n equals (EY: misc feature	ION: (98266)(98266) INFORMATION: n equals	KEY: misc_feature ION: (98343)(98343) INFORMATION: n equals	KEY: misc feature ION: (103998)(103998) INFORMATION: n equals	KEY: misc feature ION: (148948)(148948) INFORMATION: n equals	misc_feature (163385)(163385) RMATION: n equals	XEY: misc featur ION: (191989)( INFORMATION: n	misc feature (191995)(191995) %RMATION: n equals	CEY: misc featur ION: (231980)( INFORMATION: n	KEY: misc feature ION: (234187)(234 INFORMATION: n ecu	KEY: misc feature ION: (234220)(234220) INFORMATION: n equals	KEY: misc feature ION: (234814)(234814) INFORMATION: n equals	KEY: misc feature ION: (309398),.(309398) INFORMATION: n emale	KEY: misc feature TON: (309418)(309418)	INFORMATION: IL EQUALS KEY: misc feature ION: (312837) (312837)	INFORMATION: IN EQUALS KBY: misc feature ION: (312993)(312993)	<pre>fON: n equals   feature 226) (319226)</pre>	NEWATION: n equals misc_feature	: (559167)( FORMATION: n	TINFORMATION: n equals	c feature 0992)(600992) TION: n equals
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RESULT 15
US-09-422-978-2280/c
i Sequence 2280, Application US/09422978
Farent No. 6537751
GREERAL INFORMATION:
APPLICANT: Chen, Daniel
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
FILE REFERENCE: GRENET 020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT PILING DATE: 1999-10-20
EARLIER FILING DATE: 1999-10-20
EARLIER PILING DATE: 1999-10-20
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
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                                                                                                                                                                                          Query Match 77.1%; Score 16.2; DB 4; Length 1664976; Best Local Similarity 85.7%; Pred. No. 1e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0; 0
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NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-10146-202 : polymorphic base T or A
US-09-422-978-2280
; LOCATION: (1664854)..(1664855)
; OTHER INPORMATION: n equals a, t, c, or g
US-08-916-421B-1
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Search completed: May 26, 2004, 17:57:01 Job time: 42.4744 secs

42 TAAACAAAATGCATATAWTT 22

g

## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

	arch time 1940.02 Seconds (without alignments) 430.997 Million cell updates/sec
using sw model	May 26, 2004, 16:21:09 ; Search time 1940.02 Seconds (without alignments) 430.997 Million cell updat
OM nucleic - nucleic search, using sw model	May 26, 2004,
OM nucleic -	Run on:

US-10-676-299-4	28	1 caacacataaccaaaaacgcatatgatt 28
itle:	erfect score:	equence:

Scoring table: IDENTITY\_NUC Gapop 10.0, Gapext 1.0

5502657B Total number of hits satisfying chosen parameters:

27513289 segs, 14931090276 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databa

BST: *	1: em_estba:*	2: em_esthum:*	3: em_estin:*	4: em_estmu:*	5: em estov:*	6: em_estpl:*	7: em_estro:*	8: em_htc:*	  ' ;;	 14	12: gb_est3:*	 M	4: gb	 16: em_estom:*	17: em gss hum:*	B: em_
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em 558 phn: em 588 vrt: em 588 vrt: em 588 mus: em 588 mus: em 588 pho: em 588 phq: em 588 vrt: em 588 vrt: en 588 vrt: en 588 vrt: en 588 vrt: en 588 vrt: 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2G845098 1024008G0 BH370025 AG-ND-170 BH376659 AG-ND-171 BO704555 BD01 025b0
45098 70025 76658
288 738
677 400 814 154
82.9
c 1 23.2 82.9 677 12 BG8- c 2 21.6 77.1 400 28 BH3 c 3 21.6 77.1 814 28 BH3 4 21.2 75.7 154 13 BO7
4004

907 RPCI-23 131 TC3-73D 293 MBED012 995 MBED012 885 MBED012 885 MBED012 887 AVI50582 781 MBED012 781 MBED012 883 EST31752 254 PICI_11	2898 2898 2898 2898 2898 2814 281111	5342 PUHJES5T 5429 PUJB047 5427 PUJB0477 5427 PUJB0477 3346 Wus musc 3326 ZWHBB03 4719 fzmb002f 4719 fzmb002f 1485 ZWHBBD03	BU456105 60320263 AWB39294 CWO-17006 BF813601 MR2-CI018 BU497277 PEESTOADS BH255317 LDH104CR1 BB795977 BB795977 CE075035 Ligr-qss- CE671436 tigr-qss- CD643195 RF02.130P CA0946832 SCCCCL401
AZ248907 BH193131 BH989212 CG919933 BP966885 AV150582 AV150582 AV150883 AV5818781 AV585883	8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		BU436105 AW839294 BW813601 BU497277 BH255317 CE075035 CE671436 CD843195 CA094832
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497 165 670 862 1634 195 219 219 441 484	6003 6011 6011 6011 6011 6011 6011 8011 8011	888 889 977 986 1615 526 545 626 708	837 152 220 419 423 490 575 658 666
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		4.11. 4.11. 7.10. 7.00. 7.00. 7.00.	7.00.0
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2 9 0 7 7 7 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	222222222222222222222222222222222222222	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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## ALIGNMENTS

EG845098 677 bp mRNA linear EST 29-MAY-2001 1024008G02.yl C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. EG845098 EG845098.1 GI:14226282	EST. Chlamydomonas reinhardtii Chlamydomonas reinhardtii Enkaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.	Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2	Unpublished (2000) Contract: Charles Hauser Contract: Charles Hauser DOWB Box 91000 Duke University Durham, NC 27708-1000	Fax: 919 613 8177 Email: chauser@duke.edu. Location/Qualifiers
RESULT 1 BG845098/c LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM PREFERICE	AUTHORS	JOURNAL	PEATURES

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Indels

28

Length 400;

GSS 10-DEC-2001

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Contact: Brendar J Loftus
Contact: Brendar J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3543
Eax: 301 838 3543
Email: bjoftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
P.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PRST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixer ost larvae. The BAC
library was constructed at Texas AkM University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seg primer: M13 Rev
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Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
Hong,Y.S., Hogan,J.R., Carlile,J.L., Black,K., Zhang,H.-B.,
Gardmer,M.J. and Collins,P.H.
Construction of a BAC library and generation of BAC end
sequence-teaged connectors for genome sequencing of the African
malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH376658 814 bp DNA linear GSS
AG-ND-171113.TR ND-TAM Anopheles gambiae genomic clone
AG-ND-171113, genomic survey sequence.
                     /organism="Anopheles gambiae"
/organism=genomic DNA"
/strain="penomic DNA"
/strain="penomic DNA"
/db_xref="taxon:7165"
/db_xref="taxon:7165"
/clone="AG-ND-170H24"
/clone="lb="ND-TAM"
/note="Vector: pBCBAC1; Site_1: HindIII"
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Anopheles gambiae
                                                                                                                                                                                                                                                                                        Query Match 77.1%; Score 21.6; DB 28; Best Local Similarity 85.7%; Pred. No. 1.3e+03; Matches 24; Conservative 0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 CATAACATAACCAAAAAGCCATATGATT 313
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/strain="PBST"
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/clone="AG-ND-171113"
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BH376658/c
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                                                                                                                                                                                     /nce="Vector: pBluescript II SK-; Site I: BCORI; Site 2:
XhOI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDMAs from CC-1690 cells grown to
mid-log phase in TAPP (accetace-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in a
ambient levels of CO2 and HS medium bubbled with 5% CO2.
POLYA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned and cDNA
ZAP II (Stratagene) in the BCORI (5') and XhOI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exabsist (Stratagene)
phase. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806.*
                                                                                                                /db_xref="taxon:3055"
clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library efor enomic Research
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&W University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles.

(bases 1 to 400)

Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
Ren, C., Huff, R.R., Carlile, J.L., Black, X., Zhang, H.-B.,
Gardher, M.J. and Collins, F.H.

Construction of BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
malaria mosquito Anopheles gambiae

Mol. Genet. Genomics 268 (6), 720-728 (2003)
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Anopheles gambiae
Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 82.9%; Score 23.2; DB 12; Length 677; Similarity 89.3%; Pred. No. 3.4e+02; 25; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG-ND-170H24.TR ND-TAM Anopheles gambiae genomic clone
AG-ND-170H24, genomic survey sequence.
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                            organism="Chlamydomonas reinhardtii"
                                                                                 strain="CC-1690 wild type mt+ 21gr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487 chacacarachadacaccararcacr 460
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Seg primer: M13 Rev
Class: BAC ends.
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Best Local Simil
Matches 25; (
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BH370025/c
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Length 814; 77.1%; Score 21.6; DB 28;

LOCUS

RESULT 4 BQ704555 ORGANISM

VERSION KEYWORDS SOURCE

ACCESSION

REFERENCE AUTHORS

JOURNAL

TITLE

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/sex="Remale"
//lab host="DHIDB"
//clome lib="RPG1-23"
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note="Organ: Kidney/Brain; Vector: pBACe3.6
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TC3-73D19.TP TC3 Trypanosoma cruzi genomic clone TC3-73D19, genomic
Survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szladetgr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
Clone Resea ch Genetics (info@resgen.com). BAC end page:
http://www.rigr.org/rdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6 column: 7
Clones: BAC ends.
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 497)
                                                                                                                         Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mogann, S., Tsegaye, G., Geer, K., Krol, M., Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RFCI-23-57D7.TV
Contact: Shaying Zhao
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
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Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae;
Eukaryota, Buglenozoa, Kinetoplastida, Trypanosoma, Schizotrypanum.

1 (bases 1 to 165)
Kluge, S., Gadwarda, R.E., Nilsson, D., Bontempi, B.J., Myler, P., Stuart, K., Ghedin, E., El-Sayed, N.M. and Andersson, B.
Clustering and analysis of BAC-end and GSS sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21.2; DB 28; Length 497; Pred. No. 1.7e+03; 0; Mismatches 3; Indels 0;
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1. 497
/organism="Mus musculus"
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'strain="CS7BL/6J"
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/clone="RPCI-23-57D7"
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Other GSSs: TC3-73D19.TV
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Best Local Similarity 88.5%;
Matches 23; Conservative
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       Mus musculus
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BH193131/c
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                                                                                                                                                                                                                                                                                                                                           BQ704555 A 11 bp mRNA linear EST 16-JUL-2002 Bn01_02b08 A Bn01_LARC_ECORC_transgenic_Brassica_napus_overexpressing_BNCBF17_comstitutively_frost_tolerant_Brassica_napus_cDNA clone_Bn01_02b08, mRNA sequence.
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Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,
Chagnon, J., Farah, S., Couroux, P. and Hattori, J.
Expressed Sequence Tage from constitutively frost tolerant
transgenic Brassica napus overexpressing BNCBF17
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
XW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, XIA
                                    Gaps
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   Pred. No. 1.2e+03;
0; Mismatches 4; Indels
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/organism="Brassica napus"
                                                                                                                                                                  335 CATAACATAACCAAAAAGCCATATGATT 308
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Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@en.egr.ca.
Location/Qualifiers
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GSS.
Mus musculus (house mouse)
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85.78;
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   Best Local Similarity 85.7
Matches 24; Conservative
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survey sequence.
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Best Local Similarity
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CG919993
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BF966885
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/clone="rca-70319"
/clone="rca-70319"
/clone lib="rca"
/clone lib="r
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oeg91c01.gl B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.
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Contact: Bjorn Andersson
Department of Genetics and Pathology
Uppsala University
Rudbeck Laboratory, SE-751 85, Uppsala, Sweden
Tel: 46 18 471 4107
Fax: 46 18 471 4107
Fax: 46 19 471 4107
Tal: bjorn.andersson@genpat.uu.se
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: SP6
Class: BAC ends.
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Brassica oleracea
Brassica oleracea
Buxaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
I (bases I to 67)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Umpublished (2002)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mashington University School of Medicine
mail: submissions@watson.wustl.edu
Plate: oeg91 row: c column: 01
Seq primer: -28RPpOT reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Trypanosoma cruzi"
/mol_type="genomic DNA"
/strain="CL Brener"
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/organism="Brassica oleracea"
/mol type="genomic DNA"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAACACATAACCAAAAACGCATATGAT 27
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High quality sequence stop: 543.
Location/Qualifiers
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BH989212.1 GI:23526103
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Best Local Similarity
Matches 23; Conserv
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BH989212
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1634 bp mRNA linear EST 23-JAN-2001 602286560T1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4375359 3', BP966885
/clone lib="B.oleracea002"
/fnote="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the Secuencing Library prepared at Washington University Genome Sequencing Center."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Pabales, Pabaceae, Papilionoideae, Trifolieae,
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/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Cook, D.R. and Kim, D.J, unpublished"
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                                                                                                                                                                                                                                                     Length 670;
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Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                  Score 20.6; DB 28;
Pred. No. 2.6e+03;
0; Mismatches 4;
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Pred. No. 2.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/mol type="genomic DNA"
/cultivat="genotype A17"
/db_xref="taxon:3880"
/clone="33B23"
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73.6%; Score 20.6; D
Best Local Similarity 85.2%; Pred. No. 2.5e
Matches 23; Conservative 0; Mismatches
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Medicago truncatula (barrel medic)

Medicago truncatula (barrel medic)
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Seg primer: CAGGAAACAGCTATGACC
Class: BAC ends.
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1, .862
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Contact: Chris Town
                                                                                                                                                                                                                                                  ch 73.6%;
l Similarity 85.2%;
23; Conservative
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1 (bases 1 to 862)
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oshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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/clone="2900006N19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                           Genome Science Laboratory
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BG586110.1 GI:13601174
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                                    RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
                                                                                                                                                                        RIKEN
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BG586110/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="maRN*"
/db_cref="taxon:95666"
/db_cref="taxon:95666"
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/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="NIH MGC 95"
/clone lib="NIH MGC 15"
/clone li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV150582 Mus musculus hippocampus C57BL/6J adult Mus musculus cDNA clone 2900006N19, mRNA sequence.
AV150582 GI:5355788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
Bukaryota, Marazou Chordata, Craniata, Vertebrata; Euteleostomi,
Bukaryota, Merazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
1 (bases 1 to 195)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, R.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, M., Fori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nittsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shibata, T., Shipata, T., Sogabe, Y.,
Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y.,
Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procuremen: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

TOSHIYUki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLAM10040 row: h column: 16
                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria; Primates, Catarrhini, Hominidae; Homo.
1 (bases 1 to 1634)
                                                                                                                                                                                                                                       NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 72
High quality sequence stop: 252.
Location/Qualifiers
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       GI:12334100
                                                                             sapiens (human)
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                                                                                                              Homo sapiens
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Best Local 8
   VERSION
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AUTHORS
TITLE
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COMMENT
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AV150582
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ORIGIN

LOCUS

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Medicago truncatula/Glomus versiforme mixed BST library
Medicago truncatula/Glomus versiforme mixed BST library
Edwaryota; mixed BST libraries.

Edwaryota; mixed BST libraries.

I (bases 1 to 219)
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.

STS from roots of Medicago truncatula after colonization with
Glomus versiforme, 2001
U Unpublished (2001)
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Farkway, Ardmore, OK 73401
Tel: $80-221-5810
Fax: 580-221-7380
                                                                                                      Email: genome-researtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="hippocampus"
/dev_stage="adult"
/clone_lib="Mus musculus hippocampus C57BL/6J adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Noble EST name: N385173e TIGR sequence name: MTDCO14TK More
information is available at: http://www.medicago.org
Seq primer: Skmod (CTA gaA CTA gtg gAT CC).
Location/Qualifiers
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/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.4%; Score 20; DB 9; Length 195; Best Local Similarity 82.1%; Pred. No. 5.1e+03; Matches 23; Conservative 0; Mismatches 5; Indels
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
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ORIGIN

LOCUS

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Query Match
Best Local Similarity
Matches 23; Conserv
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AW585883/c
LOCUS
DEFINITION
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/tissue type="Roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post=incoulation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/lab_host="E. coli strain XLOLR"
/clone lib="WithAN"
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Xho1; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-incoulation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 441)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Hood, L., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQB18781
HS_5014_B2_D04_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=590 Col=8 Row=H, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
101 (206) 616-3618
Fax: (206) 616-3889
Fax: (206) 616-3889
Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library availability, please contact Pieter de Jong (pieter@Gejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                               ch 71.4%; Score 20; DB 12; Length 219; 1 Similarity 82.1%; Pred. No. 5e+03; 23; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 CATCACATACCCAAACATGCATATAATT 190
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/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
High quality sequence stop: 441.
Excation/Qualifiers
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Plate: 590 row: H column: B
Seq primer: SP6
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/db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ818781.1 GI:5781174
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Homo sapiens
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Best Local S:
Matches 23,
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PUBMED
COMMENT
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AQ818781
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AUTHORS
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TITLE

FEATURES

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/mol_type="mRNA"
/collivar="Medicago truncatula genotype A17"
/db_xref="taxon:11902"
/db_xref="taxon:11902"
/clone="pWHAM-39112"
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/dev stage="Roots harvested at 10, 17, 22, 31 and 38 days post-incoulation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
/lob host="B. coli strain XLOLR"
/clone lib="WHAM"
/clone lib="WHAM"
/clone lib="WHAM"
/clone lib="WHAM was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-incoulation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using GlyA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula/Glomus versiforme mixed EST library
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.

1 [Dases 1 to 484}

Harrison, M.J. liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D.,
EDWam, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
ESTS from roots of Medicago truncatula after colonization with
Glomus versiforme
U Inpublished (2000)
Contact: Maria J. Harrison
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580-221-7880
Email: miharrison@noble.org
Noble EST name: NOSABILE
TOTO CONTACT TOT
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randowly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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__ibrary"
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                                                                                                                                                                                                                                                                                                                                                    Length 441;
                                                                                                                                                                                                                                                                                                                                                         71.4%; Score 20; DB 28; iength 44 llarity 82.1%; Pred. No. 4.4e+03; Conservative 0; Mismatches 5; Indels
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More information is available at.
'http://chrysie.tawu.edu/medicago'
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 CAAAACAAAACCAAAAACCCCAATGATT 399
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us-10-676-299-4.rst

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BH187898 603 bp DNA linear GSS 29-OCT-2001 634 J 22-rev SmBAC1 Schistosoma mansoni genomic clone 034J22 5', genomic survey sequence.
                                                                                                                                                                                    Schistosoma mansoni
Schistosoma mansoni
Schistosoma mansoni
Bukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosoma.
1 (bases 1 to 603)
1 (bases 1 to 603)
1 (Pasier,M.C., Pierce,R.J., Merlin,R., Hirai,H., Wu,W.,
Hiliams,D.L., Johnston,D., Loverde,P.T. and Le Pasiler,D.
Construction and characterization of a Schistosoma mansoni
bacterial artificial chromosome library
Genomics 65 (2), 87-94 (2000)
                                                                                                                                BH187898
BH187898.1 GI:16298181
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                                                                                                                              ACCESSION
VERSION
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                                                                                         DEFINITION
                                     RESULT 15
BH187898
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COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM327254 11. B08.gl A002 Pathogen-infected compatible 1 (PIC1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 706 542 1860

Fax: 706 542 1860

Fax: 706 583 0210

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence 17 sequences, which are obtained with PolyTMix or 5eq primer: 77

Seq primer: 77

High quality sequence start: 45

High quality sequence stop: 524

POLYA=Yes.
                                                                                                                                                                                                                                      Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
I (basea I to 524)
Cordonnier-Fratt, M.-M., Gingle, A., Fang, G.C., Dean, R., King, R.,
Sudman, M. and Pratt, L.H.
An EST database from Sorghum: plants infected with a compatible
                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 .524
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Location/Qualifiers
                                                                                                                                                                                                        BM327254.1 GI:18066391
                                                                                                                                                                                                                              EST.
                                                                                                             BM327254/c
                                                                                                                                LOCUS
                                                                                                                                                                                                                                              SOURCE
ORGANISM
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AUTHORS
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KEYWORDS
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                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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299 CAACACATAATCTAACACACATATAATT 272

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Other GSSs: 034_J 22-21
Contact: Pherce RJ
Contact: Paerce RJ
INSERN U 167
Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-Lille, France
1 rue du Professeur A. Calmette, 59019-Lille, France
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877783
Fax: (33) (0)3 20877783
Fax: (33) (0)3 2087783
Fax: (34) (0)3 2087783
Fax: (35) (0)3 2087783
Fax: (35) (0)3 2087783
Fax: (35) (0)3 2087783
Fax: (37) (1)3 2087783
Fax: (38) (1)3 2087
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/lab host="Biomphalaria glabrata"
/clome lib="SmaRQ1"
/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially
/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially
/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially
/note="Vector 11 digested no hind III digested S. mansoni oercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent
sizing-ligation-transformations. Average insert size
ranges from 70-127 kb and genome coverage is 7.9-fold."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .603
/organism="Schistosoma mansoni"
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/clone="034J22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 CAACACTTTACCAGTAACACATATGATT 241
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Location/Qualifiers
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Job time : 1943.02 secs
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Best Local Similarity 82.1
Matches 23; Conservative
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Query Match 71.4%; Score 20; DB 12; Length 524; Best Local Similarity 82.1%; Pred. No. 4.3e+03; Matches 23; Conservative 0; Mismatches 5; Indels

1 CAACACATAACCAAAAAGGCATATGATT 28

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		CC924663 t078e02ba	AL097067 Drosophil	BH370025 AG-ND-170	AV382514 AV382514
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			Match Length DB ID	1 1 1 1 1 1		1101	400	571
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		14	ö	1	н	7	m	4
		Result	NO.	1	U	O	υ	υ

CD121148 ME1-0066T CG003365 ZUAET89TV EH376658 AC-ND-171 CC412273 PUHBQ8TTD AZ045495 T234126b AZ045495 T23429b AZ045518 T234299b AZ045511 T234299b AZ045511 T234299b AZ04511 T234299b AQ579547 T13503B AQ579547 T13503B BW034905 BW034905 BH989212 000991C01. BR134638 DANIO rer BH791889 SALK 0619 AL816148 AL861648 AV150582 AV150582	B276591 SALK 1378  BB737338 AU373538  BB52354 BB52354  BB7356 BB37356  BB726608 BB76608  BB16698 BB16995  A996011 vx53904 s  A994496 an32b01 J  A159538 vx80e02.r  A159538 vx80e02.r  A216537 Sheared D  A167582 vx280e02.r  A216537 Sheared D  A167582 vx93904.x  A216544 HS 3208  A1553422 vx5304  BF51845 BOHFU04TF  A55561 vx66603.r  BB551845 BOHFU04TF  A55561 vx66603.r	ENTS  p DNA linear GSS 08-AUG-2003 genomic clone t078e02ba, genomic  Craniata; Vertebrata; Euteleostomi; ccryla; Ruminantia; Pecora; Bovoidea;	Gill,C.A. and Roe,B.A. ibrary TAMBT mology Norman, OK 73019, USA
100 100 100 100 100 100 100 100	55799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56799 56	is is	33 tech 33 8 39
CG012; CG012; CG41; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04; AZ04	BEZ-66791 BEZ-65354 BEZ-2534 BEZ-2534 BEZ-2536 BEZ-2536 BEZ-2536 BEZ-2536 BEZ-2537 AZ-26537 AZ-26537 AZ-26537 AZ-26537 AZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537 BEZ-26537	A) 8 tal 02 hord etari	Adelson, loces from Benome ? Room 20
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586 698 814 817 873 863 663 663 670 670 670 671 671 671 671 672 673 673 673 673 673 673 673 673 673 673	2 5 4 8 2 8 4 8 8 8 9 8 8 9 8 9 9 9 9 9 9 9 9 9 9	.fi TAMBT E quence. 1 GI:3356 18 (cow) 18 Metazoa;	d dar,
	000000000000000000000000000000000000000	24663 3e02ba.j rey sequ 24663 24663.1 taurus taurus traurus iniyai, i	lae; Bo bases 1 5. Naj 7. Naj 11ished 11ished 1ct: Br 1ct: Br
			Bovidae 11 (bass 11 (bass Bovine) Gontact Contact Contact Contact Contact Fel: 40 Fel: 40 Fel: 40 Class: Class: High que
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11000000000000000000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 CC924663/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT
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FEATURES

Query Match

ORIGIN

Matches

CNS00Z0H/c LOCUS DEFINITION

RESULT 2

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE REFERENCE AUTHORS

COMMENT

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Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9208
Rax: 301 838 9208
This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library was generated from A. gambiae PBST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV382514 S71 bp mRNA linear EST 27-0CT-1999 AV38214 Halocynthia roretzi Fertilized egg Halocynthia roretzi CDNA clone 001L03_5 5', mRNA sequence.
AV382514
          8H370025
AG-ND-170H24.TR ND-TAM Anopheles gambiae genomic clone
AG-ND-170H24, genomic survey sequence.
                                                                                                                                                                                                                                                   1 (bases 1 to 400)
Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Gardner, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                                                                               Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halocynthia roretzi
Halocynthia roretzi
Eukaryota: Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
1 (bases 1 to 571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="AG-ND-170H24"
/clone_lib="ND-TAM"
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illarity 90.5%; Pred. No. 1.2e+03;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .400
/organism="Anopheles gambiae"
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                                                                                                                   BH370025.1 GI:17316128
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACNO1003 of DrosBAC library from Drosophila melanogaster (fruit
[IJ), genomic survey sequence.
                                                                                                                                                                                          /cell_type="Blood"
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HindlI1; TAMBI Bovine BAC library (Male) produced by Texas
A&M University, Department of Animal Science."
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (3-mail : segref@genoscope.cns.fr.
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBFH (Centre of "Etude du Polymorphisme Humanin) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Bphydroidea, Drosophilidae, Drosophila.
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Pred. No. 6.48+02;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                  87.6%; Score 18.4; DB 29; Length 774; 95.0%; Pred. No. 6.4e+02; ive 0; Mismatches 1; Indels 0
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                                                 organism="Bos taurus"
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Best Local Similarity 95.0%;
Matches 19; Conservative 0
                                                                                                                                                                          sex="Male"
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RESULT 3

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/clone="ME1-0066T-L194-C09.B"
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Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases I to S86)

1 (bases I to S86)

1 (bases I to S86)

Ojopi,E. P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.E.,
Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.E.,
Coulson,P.S., Dillon,G.P., Parias,L.P., Gregorio,S.P., Ho,P.L.,
Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
Mascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Rawano,T.,
Schistosoma,L.C., Leite,L.C.C. and Dias-Neto,E.

Transcriptome analysis of the accelomate human parasite Schistosoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Genome vas derived from the PAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/
Flate: MB1-0066T-L194 row: 9 column: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                                                                                                                                                                                                             1..571

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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84.8%; Score 17.8; DB 9; Length 571;

Best Local Similarity 90.5%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels
Makabe, K.W.
Halocynthia roretzi EST
Halocynthia roretzi EST
Unpublished (1999)
Contact: Kauuhiro W. Makabe
Department of Zoology, Graduate School of Science
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
                                                                                                                                                                                                                  Bmail: kwmakabe@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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CD121148.1 GI:34659284
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Schistosoma mansoni
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BH376658 814 bp DNA linear GSS 10-DEC-2001 AG-NN-171113.TR ND-TAM Anopheles gambiae genomic clone AG-ND-171113, genomic survey sequence.
BH376658.1 GI:17322800
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CG009365 694 bp DNA linear GSS 19-AUG-2003 ZUAET89FV ZM 3.0 4.0 KB Zea mays genomic clone ZMKBPa0045010, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 694)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Numbery, C.M., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Ocher GSSs: ZUAFT89TH
Contact: Cathy Whitelaw
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                                                                                                                                                                     / Match 84.8%; Score 17.8; DB 14; Length 586; Local Similarity 90.5%; Pred. No. 1.2e+03; Albanatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA
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Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG009365.1 GI:33881531 GSS.
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Fax: 301-838-0208
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Matches 19; Conserv
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VERSION
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Chber name. BSC-2D-030; date: 3/1/00; Submitted to the Database of
Genome Survey Sequences (GSS) on 03/13/00; More information is
available at http://chrysie.tamu.edu/medicago.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
or selected genomic DNA library"
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The Crop Blotechnology Center
Texas A&M University
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Deterson Bldg, College Station, TX 77843-2132, USA
Tel: 409 862 4790
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1 (bases 1 to 354)
Kim,D., Baek,J., Lim,H., Peng,H., Ellis,L. and Cook,D.R.
BAC survey sequencing of Medicago truncatula (2000a)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 973;
                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: Sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 84.8%; Score 17.8; DB 28; Local Similarity 90.5%; Pred. No. 1.2e+03; DB 19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula (barrel medic)
Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                    Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ045495.1 GI:7239933
                                Other GSSs: PUHBQ87TB
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Class: BAC subclone.
Unpublished (2003)
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                                                                                                    TIGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brendan J Loftus.

Contact: Brendan J Loftus.

Contact: Brendan J Loftus.

Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3543

Email: bjloftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microdganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&W Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 973 bp DNA linear GSS 19-MAY-2003 PUTAG97TD ZM 0.6 1.0 KB Zea mays genomic clone ZMWBTa414P0S, CC419273
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                                                                                                                                                                        1 (bases to 814)

Hong'X.S., Eogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,

Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B.,

Gardher, M.J. and Collins, F.H.

Construction of a BAC library and generation of BAC end

sequence-tagged connectors for genome sequencing of the African

malaria mosquito Anopheles gambiae

Mol. Genet. Genomics 268 (6), 720-728 (2003)
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                                Anopheles gambiae (African malaria mosquițo)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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84.8%; Score 17.8; DB 28; Length 814;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
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/clone="AG-ND-171113"
/clone lib="MD-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Anopheles gambiae"
/mol type="genomic DNA"
/strain="PEST"
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Class: BAC ends.
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                                                                                                                                                                     Inopheles.
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Zea mays
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CC419273/c
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/mol_type="genomic DNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
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The Crop Biotechnology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                     AZ045411.1 GI:7239849
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: pUC-C
Class: BAC subclone.
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                                                                                                                                                                             Medicago.
1 (bases 1 to 491)
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Best Local Similarity
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AQ579547/c
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/note="Vector: pUC18; BAC survey sequences were obtained
from sheared BAC DNA subcloned into the Smal site of
pUC18. The templace DNA for sequencing was obtained by PCR
sing uning universal primers. Sequencing reactions were primed
from the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA)
in the pUC18 polylinker."
                                                                                                                                                                                                                                                                                     AZ045618 11-ear GSS 14-MAR-2000 T234299b shotgun sub-library of BAC clone 12G15 Medicago truncatula genomic clone 12G15-011, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: dcook@ppserver.tamu.edu
Other name: BSC-3D-011; date: 3/1/60; Submitted to the Database of
Genome Survey Sequences (GSS) on 03/13/60; More information is
available at http://chrysie.tamu.edu/medicago.
Seg primer: pUC-D
Class: BAC subclone.
                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Trifolieae;
using universal primers. Sequencing reactions were primed from the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA) in the pUC18 polylinker."
                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Texas A&M University
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Deterron Bidg, College Station, TX 77843-2132, USA
Tel: 409 845 84790
Fax: 409 862 4790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 475)
Kim, D., Back, J., Lim, H., Peng, H., Ellis, L. and Cook, D.R.
BAC survey sequencing of Medicago truncatula (2000a)
Unpublished (2000)
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                                                                                       Length 354;
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Pred. No. 1.8e+03;
0; Mismatches 1; Indels 0
                                                                                                                          Indels
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                                                                                       28;
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/mol type="genomic DNA"
/culfivar='genocype Al7"
/db xref="taxon:3880"
/clone="12G15-011"
                                                                                    Score 17.4; DB 28.
Pred. No. 1.8e+03;
0; Mismatches 1.
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The Crop Biotechnology Center
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                                                                                82.9%;
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AZ045618.1 GI:7240056
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                                                                                                                          18; Conservative
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Best Local Similarity
                                                                                                         Local Similarity
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AZ045411
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AZ045618
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AQ579547 linear GSS 27-SEP-1999 T135008b shotgun sub-library of BAC clone 10M16 Medicago truncatula genomic clone 10-M-16-C-008, genomic survey sequence.
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T234004b shotgun sub-library of BAC clone 10M16 Medicago truncatula
genomic clone 10M16-004, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: dcook@ppserver.tamu.edu
Other name: BSC-2C-004; date: 3/1/00; Submitted to the Database of
Genome Survey Sequences (GSS) on 03/13/00; More information is
available at http://chrysie.tamu.edu/medicago.
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Supermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                   Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cook DR.
The Crop Biotechnology Center
Texas A&W University
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Peterson Bidg, College Station, TX 77843-2132, USA
Tel: 409 845 8743
Pax: 409 862 4790
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BAC survey sequencing of Medicago truncatula (2000a)
Unpublished (2000)
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BAC survey sequencing of Medicago truncatula
Unpublished (1999)
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94.7%; Pred. No. 1.8e+03;
ive 0; Mismatches 1;
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
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Best Local Similarity 94.7%;
Matches 18; Conservative (
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Matches 18; Conservative
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KEYWORDS
SOURCE
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BW034905/c
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from the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA)
in the pUC18 polylinker."
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AQ579574.1 G1:4979649
GSS.
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Pabales, Rabaces; Papilionoideae, Trifolieae,
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Fax: 409 862 4730

Fax: 409 862 4730

Ganome Survey Sequences (GSS) on 06/01/99; More information is Genome Survey Sequences (GSS) on 06/01/99; More information is Seg primer: pUC-C Class: BAC Subclone.

Location/Qualifiers
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Texas A&M University
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Peterson Bidg, College Station, Tx 77843-2132, USA
Tel: 409 845 8743
Fax: 409 862 4790
Email: dcook@appserver.tamu.edu
Other name: BSC-2-08; date: 3/3/99; Submitted to the Database of Genome Survey Sequences (GSS) on 06/01/99; More information is available at 'http://chrysie.tamu.edu/medicago'.
Class: BAC subclore.
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BAC survey sequencing of Medicago truncatula
Unpublished (1999)
Contact: Cook DR
The Crop Biotechnology Center
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Pred. No. 1.8e+03;
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94.7%; Pred
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Best Local Similarity
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AQ579574
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/Glone lib="shotgun mub-library of BAC clone 10M16" hote="Vector: pUCIB; BAC survey sequences were obtained from sheared BAC DNA subcloned into the Smal site of pUCIB. The template DNA for sequencing was obtained by PCR using universal primers. Sequencing reactions were primed from the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA) in the pUCIB polylinker."
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intestinalis cDNA clone cibd027e02 5', mRNA sequence.
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                                                                                                                                                                                                   Score 17.4; DB 28;
Pred. No. 1.8e+03;
0; Mismatches 1;
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Pred. No. 1.8e+03;
0; Mismatches 1;
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

CE 1 (bases 1 to 682)

RS Satou, Y. Satake, M., Azumi, K., Nonaka, M., Shin-i, T., Kohara, Y. and Satoh, N.

Lapressed genee in Ciona intestinalis (2002)

AL Expressed genee in Ciona intestinalis (2002)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-708-113

Email: satohasscidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

Location/Qualifiers

// organism="Ciona intestinalis"

// mol_type="mRNA"

// do xref="taxon:719"

// clone="cibd027e02"

// tissue type="blood cells"

// clone Iib="Nori Satoh unpublished cDNA library, blood cells"
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82.9%; Score 17.4; DB 13; Length 682;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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Search completed: May 26, 2004, 22:27:10 Job time : 1457.01 secs

3 ACCAMANACGCATATGATT 21

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Gaps 0

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F Thu May 27 10:11:50 2004
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GenCore version 5.1.6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query Guery Out 1 20.8 83.2 580 29 CC770012 C 2 20.2 80.8 405 28 C2455370 C 4 20.2 80.8 904 28 52499748		Description	CC770012 CH240 134 CC455370 SALK 0814 BH944102 maj94d12. BZ499748 BONGK65TR
Result Query No. Score Match Length DB 1 20.8 83.2 580 29 2 2 20.2 80.8 405 28 2 4 20.2 80.8 691 28 2 4 20.2 80.8 904 28	SUMMARIES		1
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Result NO.		Score	2000 2000 2000
		Result No.	0 0 4064

Email: h-lewin@uiuc.edu

58 SALK 0 56 sak60f 29 su72e0 62 SALK 1 12 Cm CK1 47 sak33d 9 AV53885	06404		AQ834629 HS 5442 A AG160224 Pan trog1 BB824180 GM700023A BI107403 602894488 BH083564 RFCI-24-2	n 4 m w w w w w w w	BF16.277.2 GU1709.236 CK1938.29 FGASC0224 AL286744 Tetracodon CE3666.25 tigr-gss- B08279 F5J2-T7 IGF AA165855 ms41c12.r AQ592192 HS 5434 A BU497097 PESTCab5 B1328203 602965468 B2959856 PUFJD48TB BG336309 602465230
28 BHS08958 12 BMS21656 12 BMS521656 28 CC056262 14 CD91412 14 CD91414 9 AV538859	AC .				10 BF162772 29 CK193829 29 CK186625 29 B08279 9 AA165855 28 AQ592192 13 BU497097 12 B1328203 28 B2558856 12 BG336309
0744424 0744434 0746434 074443 074443					8880000 44 4 6 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8
99.99.88 79.99.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99 79.99	9.2 76 9.2 76 9.2 76 9.2 76 76 76	9.2 76 9.2 76 9.2 76 9.2 76	20000	2244444 2444444	29.2 20.2 20.2 20.2 20.2 20.2 20.2 20.2
000	2 2 4 4 4 5 4 5 4 5 5 4 5 5 5 5 5 5 5 5				8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

RESULT 1

CC770012	
LOCUS	CC770012 580 bp DNA linear GSS 27-JUN-2003
DEFINITION	CH240 134H2.TJ CHORI-240 Bos taurus genomic clone CH240_134H2,
	genomic survey sequence.
ACCESSION	CC770012
VERSION	CC770012.1 GI:32318930
KEYWORDS	GSS.
SOURCE	Bos taurus (cow)
ORGANISM	Bos caurus
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
	Bowidae, Bowinae, Bos.
REFERENCE	1 (bases 1 to 580)
AUTHORS	Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P.,
	Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L.,
	Womack,J.E., de Jong,P.J. and Lewin,H.A.
TITLE	Bovine BAC end sequences from CHORI-240 library
JOURNAL	Unpublished (2003)
COMMENT	Other GSSs: CH240 134H2.TV
	Contact: Harris Lewin
	Department of Animal Sciences
	University of Illinois at Urbana Champaign
	1201 W. Gregory Dr., Urbana, IL 61801, USA
	Tel: 217 333 5998
	Fax: 217 244 5617

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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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KEYWORDS
SOURCE
ORGANISM
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BZ499748/c
                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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JOURNAL
COMMENT
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AUTHORS
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BH944102
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SALK_081478.48.30.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_081478.48.30.x, genomic CC455370 CC455370.1 GI:31215393
Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong [pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI [Livestock
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 405)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.8; DB 29;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.2%; Score 20.8; Dilarity 91.7%; Pred. No. 1.1e Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                         /mol type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_134H2"
                                                                                                                                                                                                                                                                                         forganism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTAAGTCATATATGTTTTGACTT 24
                                                                                                                                                                          Genome Seguencing Initiative)
Plate: 134 row: H column: 2
Seg primer: SP6
Class: BAC ends.
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1. .405
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1, .580
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Best Local Simi
Matches 22;
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DEFINITION
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CC455370/c
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KEYWORDS
SOURCE
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maj94d12.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
/clone="SALK 081478.48.30.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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/db xref="taxon:3712"
/clone llb="B.oleacea002"
/clone llb="B.oleacea002"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (Dasea I to 691)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                           Length 405;
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88.0%; Pred. No. 1.7e+03;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                     Score 20.2; DB 28;
Pred. No. 1.9e+03;
0; Mismatches 3;
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: maj94 row: d column: 12
Seq primer: -28RPpOT reverse
Class: shotgun
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High quality sequence stop: 535.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 TTATGTCATATATGTTTATGATTTA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Richard K. Wilson
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BH944102.1 GI:23424162
                                                                                                                                                                                                                                                                                                        88.08
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Best Local Similarity 88.0
Matches 22; Conservative
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Mylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Bowers, Y., Materston, R., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R., and Wilson, R.,
Unpublished (1999)
Contact: Shoemaker R/Public Soybean BST Project
Public Soybean BST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Person
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emiliar Steward.wustl.edu
This close is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BMS21656 427 bp mRNA linear BST 15-FBB-2002 sak60f04.yl Gm-c1036 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1036-7544 5' similar to TR:Q9SQU7 Q9SQU7 F24F17.7 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                          /db.caref="caraon:3702"
/clone="SAIK 051535.31.15.x"
/clone="SAIK 051535.31.15.x"
/clone="Por was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                           This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.2%; Score 19.8; DB 28; Length 370; 91.3%; Pred. No. 2.6e+03; ive 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative full length read vector to vector length is 543 Seg primer: -40RP from Gibco. Location/Qualifiers
                                                                                                                                                                                                  /mol_type="genomic_D!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 THAATTCATATATATTTTGACT 26
                                                                                                 TDNA tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTAAGTCATATATGTTTTGACT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine max (soybean)
Glycine max
                        ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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BMS21656
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DNA linear GSS 16-DEC-2002
BONGK65TR BO 1.6 2 KB tot Brassica oleracea genomic clone BONGK65,
genomic survey sequence.
                                                                                                                                                                          Brassica oleracea
Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Nagnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae; Brassica.
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Arabidopsis thaliana
Brantophyta; Unidiplanteas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis;
1 (bases 1 to 370)
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Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Bcker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /arref="taxon:3712"
/clone="BONGK65"
/clone=lib="BO. 6 2 KB tot"
/note="Vector: pH051; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pH051 using BstXI linkers"
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                                                                                                                                                                                                                                                                                                 Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Other GSSs: BONGK65TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.8%; Score 20.2; DB 28; Length 904; 88.0%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-3523
Fax: 301-838-3523
Fax: 301-838-0208
Baxi: cdcoangetyr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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Salk Institute Genomic Analysis Laboratory (SIGDAL)
The Salk Institute for Biological Studies
1010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Pax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA
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/organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="rol000DH3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.0
Matches 22; Conservative
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                                         /done liber"Gn=c1036"
//done liber"Gn=c1036"
//done libergrence: pSPORT1; Site 1: Not1; Site 2: Sal1; This conter interest was constructed from mRNA isolated from cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not1 restrictions site. Sal1 linkers adapters were ligated to the blunt-ended cDNA fragments were directionally cloned into the Not1-Sal1 restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanma at the University of Illinois at Urbana-Champaign. e-mail: l-vodkinguiuc.edu*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Channer, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Bock, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Public, Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF596529 433 bp mRNA linear EST 06-DEC-2001 su72e06.yl Gm-c1055 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1055-227 5' similar to TR:Q9SQU7 Q9SQU7 F24P17.7 PROTEIN: ;,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
Email: esfewateon.wustl.edu
Fax: 314 286 1810
Email: esfewateon.wustl.edu
Foretor to vector 1 length read
Vector to vector 1 length is 533 This clone is available through:
ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, A
35801 For further information call: {800}-533-4363 or contact via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
tissue_type="somatic embryos cultured on MSD 20"
lab host="DH10B"
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1055-227"
/tissue_type="Mature seed pods, greenhouse grown"
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91.3%; Pred. No. 2.6e+03;
ive 0; Mismatches 2;
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/mol_type="mRNA"
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BF596529
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/clone_lib="Gm-c1055"
//clone_lib="Gm-c1055"
//clone_lib="Gm-c1055"
//octor.pBluescript II SK+; Site 1: ECORI; Site 2:
XhoI; The CDNA library was constructed from makua isolated
from mature seed pods of greenhouse grown plants prior to
sensecence for the cultivar KFI. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. ECORI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The CDNA fragments were
directionally cloned into the ECORI-XhoI restriction site
of the pBluescript vector. The ligated CDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db xref="taxon:3102"
/clone="SALK_101695.17.45.x"
/clone="pck was performed on Arabidopsis thaliana lines note="pck was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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lines
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Addrinab,C., Juske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Location/Qualifiers
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Flax: 858 558 6379
Email: ecker@salk.edu
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'lab host="DH10B"
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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL COMMENT

PEATURES

REFERENCE AUTHORS

RESULT 9 CD391412/c DEFINITION

Matches

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Granda, A. Bollan, Marra, M. Hillier, L., Kucaba, T., Martin, J., Khanna, A., Bollan, Marra, M., Hillier, L., Kucaba, T., Martin, J., Khanna, A., Bollan, Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Mylie, T., Mderwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="DH10B"
//lab host="DH10B"
//lab host="DH10B"
//clone lib="Gm-c1075"
//note="Vector: pBluescript II SK+; Site I: EcoRI; Site 2:
//note="Vector: pBluescript II SK+; Site I: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from differentiating somatic embryos cultered on MSMGAC.
The library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were cransformed into E.coli BloctroMan DH10B host cells.
Tissue culture and library construction were performed by Francoise Thibaud-Nissen and Ann Khana (Lila Vodkin lab,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This close is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, At 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
BM307747 233 bp mRNA linear EST 02-JAN-2002 sak33d01.yl Gm-c1075 Glycine max cDNA clone SOYBEAN CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:3847"
/dcone="SOYBEAN CLONE ID: Gm-c1075-4777"
/tissue_type="differentiating somatic embryos cultered on
MSMGAC"
                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Pabaceae; Papilionoideae; Phaseoleae;
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    .233
/organism="Glycine max"

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Seg primer: -40RP from Gibco
High quality sequence stop: 223.
Location/Qualifiers
                                                        Gm-c1075-4777 5', mRNA sequence
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                                                                                                        BM307747.1 GI:18039453
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Institute of Genetics and Developmental Biology, CAS, China
Datun road, Beijing 100101, China
Tel: 86-10-64886859
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Soybean Ray, 2003 Sequence Tags Sequencing Unpublished (2003)
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  79.2%; Score 19.8; DB 28; 91.3%; Pred. No. 2.5e+03; ive 0; Mismatches 2;
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/mol type="mRNA"
/cultivar="Kefeng 1"
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Email: sychen@genetics.ac.cn
Seg primer: T7 primer.
Location/Qualifiers
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                                                     21; Conservative
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Gaps

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EST 07-SEP-2000

RESULT 10 BM307747/c

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ORIGIN

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Fax: 91-45-30-3018
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Sasaki,N., Izawa,M., Watahiki,M., Okazaki,Y. and
Hayashizaki,Y.
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polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
ItOh,M., Kitsunai,T., Aiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 465-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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tropicalis cDNA clone TGas080p20 3',
  Institute of Physical and Chemical Research (RIKEN)
22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="medulla oblongata"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.8%; Score 19.2; DB 9; Best Local Similarity 87.5%; Pred. No. 4.4e+03; Matches 21; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silurana tropicalis (western clawed frog)
Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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/db_xvef="taxon:10090"
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BX752631 GI:39642699
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1. .306
                      1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 262)
A samiau, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                         The Pirst Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1512-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qvalifiers
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AV518859 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cDNA clone RZ122e03F 3', mRNA sequence.
AV518859
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/clone lib="Axabidopsis thaliana roots Columbia"
/note="Vector: pBluescriptII SK-; Site_1: ScoRI; Site_2:
XRoI"
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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Pred. No. 4.5e+03;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'clone="RZ122e03F"
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                                                            AV538859.1 GI:8700615
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Kanopodinae; Silurana.

CE 1 (bases 1 to 371)

RS Croning, M.D.R., Ashurst, J.L., Taylor,R., Zorn,A.M. and Rogers,J.

AL Unpublished (2003)

Contact: Croning MDR

Sanger Kanopus tropicalis EST project 2001 (11_2003)

Contact: Croning MDR

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: tropesanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS_SRQUENCE_ID: TGas080p20.q1k77

Sequencing primer: T7

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

constructed by and Not In the 3' end.

Wector: pCS107; Site 1: EcoRI: Site_2: NotI

Host: Escherichia coli XII- blue.

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Entractary Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Entaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Entares I. (Asaes I to 441)
Entares I. (Estiman, W., Reldblyum, T., Malek, J., Shatsman, S., Akinet, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Farser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Unpublished (1999)
Contact: Shaying Zhao
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 30-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="gastrula" (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XLI-blue"
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/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 76.8%; Score 19.2; DB 13; Length 371; Best Local Similarity 87.5%; Pred. No. 4.3e+03; Matches 21; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ986840 1inear G
RPCI-23-308D20.TV RPCI-23 Mus musculus genomic clone
RPCI-23-308D20, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Silurana tropicalis"
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/db xref="taxon:8364"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="TGas080p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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GSS.
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AQ986840
LOCUS
DEFINITION
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JOURNAL
COMMENT
                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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AUTHORS
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Underson to 481)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Shoemaker, R., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Walerwook, K., Steptco, M., Thaising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCam, R., Waterston, R. and Wilson, R.

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Washington University School of Medicine
Public Soybean EST Project
Rashington University School of Medicine
Public Soybean EST Project
Rashington University School of Medicine
Full: 314 286 1800
Fax: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / dex="Pegale"
/lab host="PULOB"
/lab host="PULOB"
/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially disested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/cadeinigframe.htm) cor from Resea ch Genetics (infto@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plater: 308 row: D column: 20 Seg primer: T? Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 76.8%; Score 19.2; DB 28; Length 441; 1 Similarity 87.5%; Pred. No. 4.1e+03; 21; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. 441
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High quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTAAGTCATATATGTTTTTGACTT 24
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Glycine max
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Best Local Similarity
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Thu May 27 10:11:50 2004
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1. .481
/ organism="Glycine max"
/mol_type="mRNA"
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Xhol; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library was prepared using the Stratagene pBluescript II
XR library was prepared using the Stratagene pBluescript (dT) sequence with a Xhol restriction site. EcoRI adapters
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a Xhol restriction site of the cloned into the EcoRI-Xhol restriction site of the pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John
Erpelding."
                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
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Query Match 76.8%; Score 19.2; DB 10; Length 481; Best Local Similarity 87.5%; Pred. No. 4.1e+03; Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps

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Search completed: May 26, 2004, 22:27:15 Job time : 1737.16 secs

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2 TAAGTGATATATGTTTTTGACTTA 25

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Scoring table:

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Minimum DB Maximum DB

Database

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GSS.

Bos taurus (cow)

ENA gravota; Graniata; Craniata; Buteleostomi;

Bos taurus (cow)

Bos taurus (cow)

Bos taurus

Bovidae a Bovinae; Bos

Bovidae Bovinae; Bos

I (bases 1 to 580)

Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A.

Bovine BAC end sequences from CHORI-240 library

In Unpublished (2003)

Other GSSs: CH240 li34H2.TV

Contact: Harris Lewin

1201 W Gregory Dr., Urbana Champaign

1201 W Gregory Dr., Urbana, II, 61801, USA

Tel: 217 244 5617

Email: h-lewin@ulc.edu
BH52658 SALK 0515
BH52659 BH726064.
BF596529 BH72606.7
CC056262 SALK 1016
BM307747 BE8731601.
AV538859 AV538859
AV330260 AV330260
BM307747 BM52631
AV538859 AV538859
AV330260 AV330260
BM568294 BH10204.2
BU199436 604155121
CP075547 EST2366 Z
AZ31549 HB109436 604155121
CP075547 EST2366 Z
AZ31549 BH0032A16
BH004609 PG£1N.PK0
AQ834629 HS S442 A
AG16024 Pan troggl
BE82180 GM700023A
BH10403 604155121
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CC31212 GM MBD000
CC080116 CSU-K317.
BF168262 601773378
BH022112 GM MBD000
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BH02212 CG1773278
BH02212 CG1773278
BH02212 CG177474
AM5655 EM41C12.
AQ592122 HS S434 A
BU497097 PFESTOAB5
BH3259666 PUFJD46TB
BG336309 602405230
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CC770012.1 GI:32318930
GSS.
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                               BK521656
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CC455370 SALK 0814
BH944102 maj94d12
BZ499748 BONGK65TR
                                                                                                                                                                                 May 26, 2004, 16:21:09 ; Search time 1732.16 Seconds (without alignments) 430.997 Million cell updates/sec
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                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 US-10-676-299-10
25
1 taagtcaaaaacatatatgacttaa 25
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (bases 1 to 405)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 6539
Email: ecker@salk.edu
Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by by University of Illinois at Urbana Champalagn, USA with funds provided by grant No. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Place: 134 row: H column: 2 Seg primer: SP6 Class: BAC ends.
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/mol_type="genomic DNA"
/strain="Columbia 0"
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| /organism="Bos taurus"
| /uol_type="genomic DNA"
| strain="breed: Hereford"
| /db_xref="taxon:9913"
| /clone="CH240_134H2"
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Brassica Outeracea
Brassica Outeracea
Brassica Outeracea
Brassica Outeracea
Bermatophyta; Wagnoliophyta; endicotyledons; core endicots;
Formatophyta; Magnoliophyta; endicotyledons; core endicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (Dassa 1 to 691)
Bash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Conteact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: maj94 row: d column: 12
Seq primer: -28RPpOT reverse
Class: shotgun
High quality sequence stop: 535.
Ilocation/Qualifiers

Location/Qualifiers
/db xref="taxon:3702"
/clone="SALK 081478.46.30.x"
/clone="SALK 081478.46.30.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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//do xref="taxon:3712"
//do xref="taxon:3712"
//do foloe lib="B.olerascea002"
//note="Vector: poTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000H13 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Rablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
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llarity 88.0%; Pred. No. 1.7e+03;
Conservative 0; Mismatches 3;
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BH944102.1 GI:23424162
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BZ499748 904 bp DNA linear GSS 16-DEC-2002 BONGK65TR BO 1.6_2 KB tot Brassica oleracea genomic clone BONGK65, genomic survey sequence.
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 370)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Shinn,P., Zimmerman,J. and Bcker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Unpublished (2001)
                                                                                                                                                                                                Brassica oleracea
Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        July Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0508
Fax: 301-838-0508
Fax: 301-838-0508
Fax: 301-838-0508
Fax: 301-838-0508
Fax: 301-838-0508
Examine a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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Other GSSs: BONGK65TF
Contact: Chris Town
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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BH908958.1 GI:22721891
                                                                                                BZ499748
BZ499748.1 GI:27015132
GSS.
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/mol type="genomic DNA"
/mol type="genomic DNA"
/drain="columbia 0"
/db xref="taxon:3702"
/clone="SALK 051535.31.15.x"
/clone="Columbia 05.50.51.5."
/clone="Columbia 05.50.51.5
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Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allon, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Accan, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
71e1: 314 286 1810
Fax: 316 286 1
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Bmail: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1036-7544"
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/organism="Glycine max"
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Dupublished (1999)

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Tel: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

Vector to vector length read

Vector to vector length is 533 This clone is available through:
ResGen, Invitrogen Corp. 2330 South Memorial Parkway Huntsville, AL
35301 For further information call: (800)-533-4363 or contact via
/tissue_type="somatic embryos cultured on MSD 20"
/lab host="DH1DB"
/clone_lib="Gm-clo36"
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/note="vector: pSPORTL; Site_l: Notl; Site_2: Sall; This
cDNA library was constructed_from mRNA isolated from
somatic embryos (age ranging from 2 months to 9 months)
cultured on MSD 20. The library was prepared using the
Life Technologies pSuperScript cDNA library construction
kit. Complementary DNA was synthesized from mRNA using a
poly (dT) sequence with a Notl restrictions site. Sall
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by Notl digestion. The CDNA fragments
were directionally cloned into the Notl-Sall restriction
site of the pSPORTI vector. The ligated cDNA fragments
were directionally cloned into the laboratory of Dr. Lila
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinois at
Urbana-Champaign. e-mail: l-vodkin@uic.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF596529 433 bp mRNA linear EST 06-DEC-2001 su72e06.yl Gm-c1055 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm_c1055-227 5' similar to TR:Q9SQU7 Q9SQU7 F24P17.7 PROTEIN: ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.2%; Score 19.8; DB 12; Length 427; 91.3%; Pred. No. 2.6e+03; Live 0; Mismatches 2; Indels 0;
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Usass To 495)

Radinable: "Leisse T.J., Barajas, P., Chen, M., Cheuk, R., Gadrinable: "Leisse T.J., Barajas, P., Chen, M., Cheuk, R., Gadrinable: "Jemmerman, J. and Bcker, J.R., Kim, C.J., Parker, H., Prednis, L., Shirm, P., Zimmerman, J. and Bcker, J.R., A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

A. Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

A. Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome

A. Sequence Insertion Genomic Analysis Laboratory (SIGnAL)

The Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Instit
/lone lib="da-c1055"
//lone lib="da-c1055"
//lone lib="da-c1055"
//lone lib="da-c1055"
//lote="Vector: pBluescript II SK+; Site 1: BcoRI; Site 2:
XhoI; The CDNA library was constructed from mRNA isolated
from mature seed pods of greenhouse grown plants prior to
senescence for the cultivar XPI. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly (dT) sequence with a XhoI restriction site. BcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The CDNA fragments were
followed by XhoI digestion. The CDNA fragments were
followed by XhoI digestion. The Income is the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SALK 101695.17.45.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_101695.17.45.x, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/mol_type="genomic DNA"
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 AACTCAAAACATAGATGACTTA 369
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CC056262.1 GI:29475926
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Query Match Best Local

Matches

ઠે 원 VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 9 CD391412 LOCUS

ACCESSION

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from differentiating somatic embryos cultered on MSM6AC.
The library was prepared using the Stratagene pBluescript
II SK(+) library construction Kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an XhoI restriction site. EcoRI
adaptors were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the ECORI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into E.coli ElectroMax DHIOB host cells.
Tissue culture and library construction were performed by
Francoise Thibaud-Nissen and Ann Khana (Lila Vodkin lab,
University of Illinois)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shoemaker R/Public Soybean BST Project
Public Soybean BST Project
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
1314 286 1800
Fax: 314 286 1800
Bmail: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
BM307747 2002 233 bp mRNA linear EST 02-JAN-2002 sak33d01.y1 Gm-c1075 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1075-4777 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mkha"
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/clone="sOYBEAN CLONE ID: Gm-c1075-4777"
/tissue_type="differentiating somatic embryos cultered on
MSM6AC"
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                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Pabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                         Changes 1 to 233)
Shommaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shomma, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J.,
Khanna, A., Bolla, B., Marra, M., Hiller, L., Theising, B., Allen, M.
Bock, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.
Bowers, Y., Person, S., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.8%; Score 19.2; DB 12; Length 233; 87.5%; Pred. No. 4.6e+03; ive 0; Mismatches 3; Indels 0;
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    .233
/organism="Glycine max"

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High quality sequence stop: 223.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAAGTCAAAACATATATGACTTA
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                                                                                                                               BM307747.1 GI:18039453
                                                                                                                                                                                                Glycine max (soybean)
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                                                                                                                                                                                                                                 Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
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AV538859
LOCUS
                   LOCUS
                                                                                                                                                                                                                                 ORGANISM
                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
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/dev_stage="xtwo-week settings"
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/clone_lib="soybean induced by Salice_1: EcoR I; Site_2:
/clone_lib="soybean induced by Salicylic acid for 24, 36, 48
and 72 h. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dr) sequence with a
xhol striction site. EcoR1 adapters were ligated to the
blunt-ended CDNA fragments followed by Xhol digestion. The
CONA fragments were directionally cloned into the
EcoR1.Xhol restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into XL1-Blue MRP'
host cells (Stratagene)."
                                                                                                                                                                                                                                                                                                                                  CDJ91412 666 bp mRNA linear EST 01-JUN-2003 Gm ck10293 Soybean induced by Salicylic Acid Glycine max cDNA 3', mRNA sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Pabales, Fabaceae, Papilionoideae, Phaseoleae,
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                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tienes 1 to 666)
Tien, A.-G., Wang, J., Cui, P., Han, Y.-J., Xu, H., Cong, L.-J., Huang, X.-G., Wang, J., Cui, P., Han, Y.-J., Xu, H., Cong, L.-J., Huang, X.-G., Wang, X.-S., Chen, S.-Y. and Yu, J. Soybean Expressed Sequence Tags Sequencing Unpublished (2003)
Unpublished (2003)
Enact: Chen S.-Y.
Plant Biotechnology Laboratory
Institute of Genetics and Developmental Biology, CAS, China Datun road, Beijing 100101, China
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79.2%; Score 19.8; DB 14; Length 666;
Best Local Similarity 91.3%; Pred. No. 2.4e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0
                   Length 495;
                                                                                 2; Indels
                   79.2%; Score 19.8; DB 28; 91.3%; Pred. No. 2.5e+03; tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                                                                                                      224 inagicandachchininingir 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: sychen@genetics.ac.cn
Email: sychen@genetics.ac.cn
Seq primer: 17 primer.
Location/Qualifiers
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                                                                                                                                            1 TAAGTCAAAACATATATGACTT 23
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                                                                                 21, Conservative
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                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max
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FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS 07-SBP-2000

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BX752631 XGC-gastrula Silurana tropicalis CDNA clone TGas080p20 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site 1: Sall; Site 2: Bamil; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer [3], cDNA was GAGAGAGAGAGCCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                          Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M.; Kitsunai, T.; Akiyama, J.; Shibata, K., Izawa, M.; Kawai, J., Caranici, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Aucomated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lib="RIKEN full-length enriched, adult male medulla
                             Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,.,, Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rissue_type="medulla oblongata"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silurana tropicalis (western clawed frog) Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX752631.1 GI:39642699
                                 1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oblongata"
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Best Local Si
Matches 21;
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BX752631
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

[2] (Dases 1 to 306)

[3] (Dases 1 to 306)

[4] Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, B., Endo, T., Fukuda, S., Fukuda, S., Fukuda, S., Akiyama, J., Tabawa, M., Kadota, K., Kadota, K., Kadota, T., Kai, C., Yawai, J., Xikuchi, N., Yohm, Y., Kodota, K., Kadawa, T., Kai, C., Yawai, J., Xikuchi, N., Kojima, Y., Koda, H., Okazaki, Y., Matuo, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Yakuda, T., Yakudi, H., Yakudahi, F., Tateno, M., Tominaga, N., Suzuki, H., Yakudahi, F., Tateno, M., Tominaga, N., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Unpublished (1999)
                                                                                                                                                                                                                                                   Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacee; Arabidopsis.

1 (bases I to 263)
Asamiru,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of I2,028 non-refundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV330260 RIKEN full-length enriched, adult male medula oblongata Mus musculus CDNA clone 6330512K13 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Criba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="R212ctols"
/clone="R212ctols"
/clone lib="Arabidopsis thaliana roots Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
Xhol:
       AV538859 Arabidopsis thaliana roots Columbia Arabidopsis thaliana COLDA clone RZ122e03F 3', mRNA sequence. AV538859.1 GI:8700615
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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Pred. No. 4.5e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis chaliana"
                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="Columbia"
/db_xref="taxon:3702"
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Mus musculus
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AV330260.1 GI:6370312
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Best Local Similarity 87.5%;
Matches 21; Conservative
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                                                                                                                           VERSION
KEYWORDS
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AV330260
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                                                                                                                                                                                                                                    Email: tropdesinger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_ESQUENCE_ID: TGas080p20.q1kT7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
GDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13
gastrulae. ECORI-NotI cut cDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site 2: NotI
HGST: Escherichia coli XII- blue.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bukaryota, Eutheria; Rodentia, Sciurognathi, Muridae, Musinae, Mus. 1 (Jases 1 to 41)

Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Karnet, B., Levinas, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Mouse BAC End Sequences from Library RPCI-23

Other GSSs: RPCI-23-308D20, TJ

Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Bscherichia coli XL1-blue"
/clone lib="XGC-gastrula"
/note="Wector: pCS107; Site 1: EcoRI; Site 2: MotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.

I (bases 1 to 31)

Croning,M.D.R., Ashurat,J.L., Taylor,R., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis BST project 2001 (11_2003)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RPCI-23-308D20.TV RPCI-23 Mus musculus genomic clone RPCI-23-308D20, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Silurana tropicalis"
/mol_type="mkNA"
/db_xref="taxon:8364"
/clone="TGas080p20"
                                                                                                                                                                                                                   Hinxton, Cambridgeshire, CB10 1SA, UK
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Mus musculus
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                                                                                                                                                                         Contact: Croning MDR
                                                                                                                                                                                            Sanger Institute
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AQ986840/c
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/lab host="Penale"
//lab host="DHIOB"
//lab host="DHIOB"
//lab host="DHIOB"
//lab host="DHIOB"
//lab host="Corgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note="Organ: Kidney/Brain; Venale C57BL/6f mouse Kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BHIOB electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker, R. Keim, P., Vodkin, L., Brpelding, J., Coryell, V.,
Shoemaker, R., Keim, P., Vodkin, L., Brpelding, J., Kucaba, T., Martin, J.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Bock, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Public, Soybean, EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1046 Std Brror: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AM#3bVJU7 481 bp mRNA linear BST 03-DBC-2001 sh12f03.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-4566 5', mRNA sequence.
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library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea of Genetics (info@resgen.com). BAC end page.
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 76.8%; Score 19.2; DB 28; Length 441; 1 Similarity 87.5%; Pred. No. 4.1e+03; 21; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                             1. .441
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                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/61"
/db_xref="taxon:10090"
/clone="RPCI-23-308D20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40RP from Gibco
High quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 AAGTGGAAACATATTGACTTAA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AAGTCAAAACATATATGACTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW458707.1 GI:7028924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max (soybean)
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source
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/organism="Glycine max"
/wol type="mRNA"
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ORIGIN

Ouery Match 76.8%; Score 19.2; DB 10; Length 481; Best Local Similarity 87.5%; Pred. No. 4.1e+03; Matches 21; Conservative 0; Mismatches 3; Indels 0;

0; Gaps

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1 TAAGTCAAAACATATATGACTTA 24

Д δ

Search completed: May 26, 2004, 22:27:15 Job time: 1732.16 secs

H

using sw model OM nucleic - nucleic search,

May 26, 2004, 15:22:28; Search time 164.244 Seconds (without alignments) 594.900 Million cell updates/sec Run on:

US-10-676-299-7 23 1 ttaatcatatgcgtttttggtta 23 Title: Perfect score: Sequence:

Scoring table:

3373863 segs, 2124099041 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003bs:\*geneseqn2003cs:\* N\_Geneseq\_29Jan04:\* 1: geneseqn1980s:\* geneseqn2003as:\* genesegn2004s:\* geneseqn1980s:\* geneseqn1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Acd28588 E. coli A	Acd28584 E. coli A	Acd28589 E. coli A	Acd28585 E. coli A	Ada53054 Human cod	Aaf28554 Genomic f	Able7877 Human ova	Abn92532 Staphyloc	Abx11.841 Bacillus	Ade71408 Bacillus				Aaa97493 Bacillus		Aag27180 Alkaline	Abl33694 Human imm	Abn80210 Human che	Continuation (13 o	Aca44727 Prokaryot			Abq42336 Oligonucl
SUMMARIES	QI	ACD28588	ACD28584	ACD28589	ACD28585	ADA53054	AAF28554	ABL87877	ABN92532	ABX11841	ADE71408	AA169288	AAN70651	ABZ57796	AAA97493	AB257797	AAQ27180	ABL33694	ABN80210	AAT42063_12	ACA44727	AAS05443	ABQ42337	ABQ42336
	DB		8	œ	œ	7	4	9	9	7	σ	9	æ4	۲-	ċή	7	~	ω	φ	N	~	Ŋ	φ	9
	Query Match Length DB	23	30	21	29	3727	269223	343	1026	2322	2475	2783	2923	3150	3189	3332	3463	10717	10717	110000	1371	627	639	639
*	Query	100.0	100.0	91.3	91.3	81.7	81.7	79.1	79.1	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	75.7	74.8	74.8	74.8
	Score	23	23	21	21	18.8	18.8	18.2	18.2	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.4	17.2	17.2	17.2
	Result No.	1	7	რ ს	Ω	C C	9	7	<b>ω</b>	Ω Φ	0 10	0 11	c 12	0 13	c 14	c 15	c 16	17	18	c 19	20	c 21	c 55	23

	Abz14902 Arabidops	Abl32346 Human imm	Abl34458 Human met	Abk31504 Signal tr	Abl70475 Chemicall	Aas61438 Human gen	Abl33406 Human imm	Aaa81455 N. mening	Aak86476 Human imm	Continuation (15 o	Continuation (14 o	Continuation (3 of	Aaf21610 Neisseria		Aaq67726 Comamonas	Ab132255 Human imm	Aak53769 Murine tr	Abv31693 Human pro	Abv40661 Human pro	Aah94140 Human foe	Ada29013 DNA encod
AAP54914	ABZ14902	ABL32346	ABL34458	ABK31504	ABL70475	AAS61438	ABL33406	AAA81455	AAK86476	AAA81490 14	AAA81490 13	ABQ83210_2	AAF21610	AAQ36874	AAQ67726	ABL32255	AAK53769	ABV31693	ABV40661	AAH94140	ADA29013
4	9	9	9	v	vo	ω	w	m	4	'n	m	_	m	N	N	ø	4	'n	'n	S	œ
1257	2000	5216	5216	7843	7843	7843	8423	23532	27804	37668	110000	110000	349980	3658	1491	18154	318	352	352	453	459
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74	74	74	74	74.	74	74.	74.	74.	7.4	74.	74.	74.8	74	73	73	73	7.2	72	72	72	72
17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17,2	17.2	17.2	17	16.8	16.8	16.6	16.6	16.6	16.6	16.6
4	23	56	22	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

BP ACD28588 standard; DNA; 23 (first entry) 10-OCT-2003 ACD28588; RESULT 1 ACD28588 

E. coli ArsR binding oligonucleotide PLASSIT.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003.

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

(LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte, (2) an isolated nucleic acid containing a specifically binding sequence that is bound specifically by the protein, and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the arsenic resistence operon of S. coli) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid

Indels

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sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyre in a sample. The present sequence is the top strand of an oligonucleotide which binds to plasmid expressed Arsk protein and is used in the biosensor of the
88888888
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Sequence 23 BP; 5 A; 2 C; 4 G; 12 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 23; DB 8; Length 23; 100.0%; Pred. No. 1.6; ive 0; Mismatches 0; Indels 23; Conservative Local Similarity Query Match Matches

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1 TTAATCATATGCGTTTTTGGTTA 23

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TTAATCATATGCGTTTTTGGTTA 23

RESULT 2 ACD28584

BP ACD28584 standard; DNA; 30

ACD28584;

(first entry) 10-OCT-2003

E. coli Arsk binding oligonucleotide PLASLIT.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

(LAIN/) LAING L G.

Laing

WPI; 2003-576876/54.

system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample. system comprising isolated protein and nucleic acid, and a detection

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein (2) a detection system that indicates a change in binding of the protein (2) a detection system to resence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and an Arsk (encoded by part of the arsenic resistance operon of B. coli) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as ABG3440 binding to a nucleic acid sequence appearing as ABG3440 binding to a nucleic acid sequence appearing the presence of analyte in a sample. The present sequence is the top strand of an oligonucleotide which binds to a planning expressed Arsk protein and is used in the biosensor of the 

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23

3 AATCATATGCGTTTTTGGTTA

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ACD28588/c ID ACD28585 standard; DNA; 28 BP.

RESULT

Seguence 30 BP; 5 A; 2 C; 7 G; 16 T; 0 U; 0 Other;

Score 23; DB 8; Length 30; Pred. No. 1.6; 100.0%; Query Match Best Local Similarity

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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and an Arsk (encoded by part of the arsenic resistence operon of E. coll) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as ABUG3440 binding to a nucleic acid sequence comprising oligonucleotides appearing as ABUG38564-ABUZ8691. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds is the bottom strand of an oligonucleotide which binds is increased Arsk protein and is used in the biosensor of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.
 Gaps
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                                                                                                                                                                                                                                                                                                           ArsR; arsenic resistance operon; biosensor; ss; arsenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 10 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                           B. coli ArsR binding oligonucleotide PLASSIB.
 Mismatches
                                     23
                                                                      23
                                                        TTAATCATATGOGTTTTTGGTTA
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                                                                                                                       RESULT 3
ACD28589/c
ID ACD28589 standard; DNA, 21
                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 100.
Matches 21; Conservative
 23; Conservative
                                     TTAATCATATGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPI; 2003-576876/54.
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                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                     JS2003096275-A1.
                                                                                                                                                                                                                                        10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-2003
                                                                                                                                                                                                     ACD28589;
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 Matches
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Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF28554/c
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the mucleic acid in the presence of the analyte. Also included are a biosensor device for an analyte in a sample, at a cample, and an Arsk (encoded by part of the arsenic resistance operon of E. coll) protein comprising an amino acid sequence appearing as ABU63440 binding to a mucleic acid sequence appearing as ABU63440 binding to a mucleic acid sequence comprising oligonucleorides appearing as ACD28581. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleoride which binds to a plasmid expressed Arsk protein and is used in the biosensor of the
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                                                                                                                                                                                                                                                                               New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; Anti-inflammatory, Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 8; Length 28; Pred. No. 11;
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                                                                          ArsR; arsenic resistance operon; biosensor; ss; arsenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28 BP; 14 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%; Scor.
100.0%; Pred. No. ...
                                                     E. coli ArsR binding oligonucleotide PLASLIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human coding sequence, SEQ ID 622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AATCATATGCGTTTTTGGTTA 23
                                                                                                                                                                                                                                                                                                                                      Claim 35, Page 15, 36pp, English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 Aarcarargcerrirregira 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA53054 standard; cDNA; 3727
                                                                                                                                                                  15-AUG-2002; 2002US-00222952
                                                                                                                                                                                        20-AUG-2001; 2001US-0313714P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guery Match
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Best Local 21; Conservative
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                  analyte in a sample.
                                                                                                                                                                                                              (LAIN/) LAING L G.
                                                                                                Escherichia coli
                                                                                                                       US2003096275-A1
                              10-0CT-2003
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                                                                                                                                             22-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                     Laing LG;
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         ACD28585;
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ADA53054/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                  Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic library; bacteria; human upper airway; otitis media; sinusitis;
bronchopulaonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel human secretory or membrane proceins (ADAS4072-ADAS5710) and their coding sequences (ADAS433-ADAS401). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3727 BP, 927 A; 839 C; 1016 G; 945 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 622; 205pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF28554 standard; DNA; 269223 BP.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                             21-MAR-2002; 2002EP-0006586.
                                                                                                                                                                      14-SEP-2001; 2001JP-00328381, 24-JAN-2002; 2002US-0350435P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 90.5
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lagace RE, Patterson C,
                                                                                                                                                                                                                                                                                                                                                     Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic fragment #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-395539/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-041427/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ADA54693.
EP1293569-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000.
                                                        19-MAR-2003
                                                                                                                                                                                                                                                                                                                                                     Isogai T,
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The present invention relates to a Moraxella catarhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarhalis (Branhamella catarhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarhalis is known to cause acute, localised infections such as otticis media, sinustis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                   Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids.
                                                                                                                             Claim 1; Page 486-545; 545pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                and meningitis
```

Sequence 269223 BP; 77067 A; 56596 C; 57380 G; 78180 T; 0 U; 0 Other;

Gaps ch 81.7%; Score 18.8; DB 4; Length 269223; L Similarity 90.9%; Pred. No. 1.2e+02; 20; Conservative 0; Mismatches 2: Indels n. Query Match Best Local Similarity Matches

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ABL87877;

17-MAY-2002

H H

ABL87877 standard; cDNA; 343

Human ovarian cancer related cDNA clone SEQ ID NO:10855.

Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

Homo sapiens.

W0200192581-A2.

06-DEC-2001.

29-MAY-2001; 2001WO-US017756.

26-MAY-2000; 2000US-0207484P.

(CORI-) CORIXA CORP

SL, Algate PA, Harlocker

Jones R;

WPI; 2002-122075/16.

Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polymucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.

Claim 1; SEQ ID NO 10855; 489pp; English

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polymucleotide (III) having a cDNA sequence (SI) from the 10912 nucleotide sequences as given in ABL/7023 to ABLB/7934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological 

sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting to isolate a full length gene from a suitable library e.g., a tumour cells; and library using well known techniques

88888888888888

Sequence 343 BP; 117 A; 52 C; 50 G; 124 T; 0 U; 0 Other;

Gaps ö 79.1%; Score 18.2; DB.6; Length 343; 87.0%; Pred. No. 1.9e+02; 3; Indels 0; Mismatches Local Similarity 87.0 nes 20; Conservative Query Match **datches** 

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TTAATCAGATGCCTTTTTAGTTA 100 1 TTAATCATATGCGTTTTTGGTTA 23

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BP. ABN92532 standard; DNA; 1026

24-JUL-2002 ABN92532;

Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1995

Staphylococcus epidermidis, open reading frame; ORF; bacterial infection, antibacterial; gene therapy; gene; ds.

Staphylococcus epidermidis

US6380370-B1

30-APR-2002,

98US-00134001 13-AUG-1998;

97US-0055779P. 97US-0064964P. 14-AUG-1997; 08-NOV-1997;

THERAPEUTICS CORP. (GENO-) GENOME

Bush D; Doucette-Stamm LA,

WPI; 2002-381255/41. P-PSDB; ABP39987 Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections

Disclosure; SEQ ID NO 1995; 267pp; English.

ABN99538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site 

Sequence 1026 BP; 369 A; 124 C; 231 G; 302 T; 0 U; 0 Other;

Query Match

DB 6; Length 1026; 79.1%; Score 18.2; S

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The invention relates to an enzyme exhibiting endo-beta-1,4-glucanase activity (EC 3.2.1.4), comprising: (a) a polypeptide encoded by the DNA sequence appearing as ABX11841; (b) a polypeptide produced by culturing a cell comprising the DNA sequence under conditions where the DNA sequence is expressed; (c) an endo-beta-1,4-glucanase enzyme having at least 97% sequence identity to the amino acid sequence appearing as ABG76403; or (d) a polypeptide having endo-beta-1,4-glucanase activity that is encoded by a polymucleotide that hybridizes to the DNA under hybridisation conditions comprising 5X SC at 45 plusoc and washing conditions comprising 5X SC at 45 plusoc and washing conditions comprising by a polymucleotide construct comprising may of the DNA sequence, a polymucleotide construct comprising any of the DNA sequence.

The expression vector (comprising the following operably linked elements: a transcription terminator), a cultured cell comprising the vector and compressing the enzyme, a method for degradation of cellulose-containing biomass that is treated with the enzyme or enzyme composition cited above and a hybrid endo-glucanase (exhibiting endo-beta-1,4-glucanase activity comprising the cellulase binding domain, CBD, of the enzyme, and a catalytic domain (CAD) from sources other than Bacillus sp. AA349 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New enzyme exhibiting endo-beta-1,4-glucanase activity, useful in detergent compositions, oil industry textile finishing processes, biomass degradation, laundry, and stone washing.
                                                                                                                                                                                                                                                                                                                                          Gene, ds; endo-beta-1,4-glucanase; detergent; textile finishing process; oil industry; biomass degradation; laundry; stone washing; pulp processing; animal feed.
                   Gaps
                   ö
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /EC_number= "EC 3.2.1.4"
/product= "Endo-beta-1,4-glucanase"
/partial
                                                                                                                                                                                                                                                                                                             Bacillus sp. DNA encoding endo-beta-1,4-glucanase.
                   س
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibson
Pred. No. 2e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "No start codon shown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eskelund MB,
                                                                      624 TAATCATATGCTTTTTAGTTA 602
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus sp; AA349 strain DSM 12648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                    1 TTAATCATATGCGTTTTTGGTTA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 42-45; 51pp; English.
                                                                                                                                        Best Local Similarity 87.0%;
Matches 20; Conservative (
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The invention relates to a mutant alkaline cellulase derived from the Bacillus sp. KBM-S237 alkaline cellulase Bg1-237 (ABS71407). The mutant enzyme is created by deleting one or more amino acid residues between residues 343-373 of the wild-type enzyme, and then inserting a 2-15 residue peptide into the deletion site. The invention also encompasses a gane encoding a mutant alkaline cellulase of the invention, and vectors and host cells comprising a matent alkaline cellulase-encoding gene. The wery close to the pu of laundry water (around pil 10.5) and are therefore useful as enzymes for detergents. The present sequence represents the gene encoding wild-type Bacillus sp. KSM-S237 alkaline cellulase Eg1-237.

Mutated alkaline cellulase for use as an enzyme for detergents is produced by deleting one or more amino acid residue groups from the 3·to 3/3-positions in SEQ ID No:1 and then inserting a peptide into the

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Kobayashi

Ozawa T,

Hakamada Y,

(KAOS ) KAO CORP

WPI; 2003-854397/79.

P-PSDB; ADE71407

25-APR-2003; 2003WO-JP005371. 25-APR-2002; 2002JP-00124474 Disclosure; SEQ ID NO 2; 31pp; Japanese.

deletion site.

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DSM12648). The enzymes are useful in detergent composition, textile finishing processes, oil industry, biomass degradation, laundry and stone washing. The invention provides enzymes having substantial beta-1,4-glucanase activity under slightly acid to alkaline conditions and improved performance in pulp processing, textile treatment, laundry processes, extraction processes or in animal feed. The present sequence encodes the endo-beta-1,4-glucanase. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                             Alkaline cellulase; Eg1-237; wild-type; mutant enzyme; detergent;
                                                                                                                                                                                                                                                                                         KSM-5237 alkaline cellulase Egl-237-encoding gene.
                                                                                                                                    ö
                                                                                            Sequence 2322 BP; 774 A; 374 C; 546 G; 627 T; 0 U; 1 Other;
                                                                                                              77.4%; Score 17.8; DB 7; Length 2 90.5%; Pred. No. 2.9e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                               2015 TTAATCGTATACGTTTTTGGT 1995
                                                                                                                                                        1 TTAATCATATGCGTTTTTGGT 21
                                                                                                                                                                                                          RESULT 10
ADE71408/c
ID ADE71408 standard; DNA; 2475 BP.
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                        Local Similarity 90.5
                                                                                                                                                                                                                                                                                                                                            Bacillus sp. KSM-S237.
                                                                                                                                                                                                                                                                                                                        laundry; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003091422-A1.
                                                                                                                                                                                                                                                                                          Bacillus ap.
                                                                                                                                                                                                                                                                       29-JAN-2004
                                                                                                                                                                                                                                                    ADE71408;
                                                                                                                 Query Match
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No. 1139

(revised)
(first entry)

Location/Qualifiers

/\*teg= a /\*teg= a 203..292 /\*teg= b 293..2605 /\*teg= c 2690..2706 /\*teg= e /\*teg= e

86JP-00076285 B6JP-00076285

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By using this DNA sequence cellulase can be produced. This cellulase hydrolyses cellotriose or cellotetrose and does not hydrolyse cellobiose. Molecular weight is approx. 92K dalton and optimum pH is 9. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence coding cellulase gene - is derived from Bacillus sp. z and can hydrolyse cello-triose and cello-tetrose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2923 BP; 992 A; 455 C; 654 G; 822 T; 0 U; 0 Other;
                                   Sequence of cellulase gene derived from Bacillus sp.
                                                             Enzyme; cellotriose; cellotetrose; hydrolysis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3-1 - 3-3; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                 (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                        Bacillus sp; No. 1139.
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1987-325245/46.
                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAP70420
                                                                                                                                                                                                                                       misc_structure
                                                                                                                                                                                                            misc_structure
                                                                                                                                                                                                                                                                                                                               02-APR-1986;
                                                                                                                                                                                                                                                                                                                                                       02-APR-1986;
                                                                                                                                                                                                                                                                            JP62232386-A
24-0CT-2003
20-JAN-1991
                                                                                                                                                                                                                                                                                                      12-0CT-1987.
                                                                                                                                                                                    mat_peptide
                                                                                                                    Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel alkaline cellulase gene from a Bacillus sp. The alkaline cellulase gene is used for the preparation of an aklaline cellulase useful as a textile detergent and a textile treating agent. This sequence encodes the Bacillus sp. alkaline cellulase N131b described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alkaline cellulase gene useful for the preparation of an alkaline cellulase useful as a textile detergent and a textile treating agent.
                                                                    Gaps
                                                                                                                                                                                                                                                                                            Alkaline cellulase; N131b; textile; detergent; treating agent; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

77.4%; Score 17.8; DB 6; Length 2783;
Best Local Similarity 90.5%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                   ö
                                        Query Match 77.4%; Score 17.8; DB 9; Length 2475; Best Local Similarity 90.5%; Pred. No. 2.9e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2783 BP; 925 A; 468 C; 635 G; 755 T; 0 U; 0 Other;
                Sequence 2475 BP; 838 A; 394 C; 574 G; 669 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "alkaline cellulase N131b"
/transl_except= {pos:326. .328,aa:frp}
                                                                                                                                                                                                                                                                   Bacillus sp alkaline cellulase N131b encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 15-18; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
293. .2734
                                                                                                           2102 TTAATCGTATACGTTTTTGGT 2082
                                                                                               21
                                                                                                                                                                                        AA169288 standard; DNA; 2783 BP
                                                                                               1 TTAATCATATGCGTTTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-2000; 2000JP-00047237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2000; 2000JP-00047237
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-029359/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAG80267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAOS ) KAO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                              JP2001231569-A
                                                                                                                                                                                                                                           08-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001
                                                                                                                                                                                                                                                                                                                        Bacillus sp
                                                                                                                                                                                                                   AA169288;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:1
                                                                                                                                ö
Query Match
Best Local Similarity 90.5%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus sp. XSM-S237 sporulation-associated gene #1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
573. .3047
                                                                                                                                                                                                                                                          ABZ57796 standard; DNA; 3150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus sp. KSM-S237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ57796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
ABZ57796/A
NX ABZ5
XX
AC ABZ5
XX
XX
DT 16-A
DT 16-A
DT XX
SPOOT
X
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Gaps

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PAN70651 standard; DNA; 2923 BP

RESULT 12 AAN70651/ ID AAN7 AAN70651;

3

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no 1139

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rbu May 27 10:11:45 2004
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99JP-00013049.

21-JAN-1999; 21-JAN-1999;

02-AUG-2000.

WPI; 2000-596504/57. (KAOS ) KAO CORP.

P-PSDB; AAB23180

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The invention relates to microorganisms (particularly Bacillus species)

in which one or more sporulation-associated genes active in the medium to
latter stages of sporulation have been deactivated or deleted. Such genes
include the sigE, sigF, spoilE, spoilEs, sigG, spoiVCB and spoilE genes
include the sigE, sigF, spoilEs, sigG, spoiVCB and spoilE genes

the invention also relates to the recombinant production of a protein

the invention are incapable of producing spores, recombinant protein

production is more efficient, with reduced formation of by-products,

teduced energy loss, reduced consumption of culture medium, and increased

speed of target protein production. In addition, protein production can
be efficiently carried out over a longer period of time than is currently
the case. The microorganisms can be used to recombinantly produce target

proteins for use in a variety of applications, such as in foodsruffs,
drugs, cleaning agents and toiletries. The present sequence represents a

satillus sp. KSM-S237 sporulation-associated gene related to the
live invention. Note: The present sequence is siting,
but is not further referred to in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus strain having genes associated with sporulation inactivated for use as hosts in more efficient production of recombinant proteins.
/*tag= a /prorulation-associated protein #1" /product= "Sporulation-associated protein #1" /product= "Sporulation-associated protein #1" /product= "Mature sporulation-associated protein #1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3150 BP; 1073 A; 474 C; 695 G; 908 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          Tohata M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14-19; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                          Ozawa I,
                                                                                                                                                                                                                                                   28-MAY-2002; 2002WO-JP005151
                                                                                                                                                                                                                                                                                           29-MAY-2001; 2001JP-00160520
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-140463/13.
P-PSDB; ABP58992.
                                                                                                                                                                                                                                                                                                                                                                          Sawada K, Endo K,
                                                                                                                                                                                                                                                                                                                                  (KAOS ) KAO CORP
                                                                                                                                                                W0200297064-A1
                                                                                                                                                                                                            05-DEC-2002
                                                                                 mat_peptide
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Ozaki K;

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Gaps
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Query Match 77.4%; Score 17.8; DB 7; Length 3150; Best Local Similarity 90.5%; Pred. No. 3e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                             2674 TTAATCGTATACGTTTTTGGT 2654
                                                                                     1 TIAATCATATGCGTTTTTGGT 21
                                                                                                                     g
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493/c AAA97493 standard; DNA; 3189 BP. 29-JAN-2001 (first entry) AAA97493 

Bacillus sp. KSM-S237 heat resistant alkaline cellulase DNA.

Heat resistant alkaline cellulase; detergent; cleaning application; ds.

Bacillus sp. KSM-S237.

JP2000210081-A

ö The invention relates to a novel heat resistant alkaline cellulase (AAB23180) from Bacillus sp. KSM-S237, and to the gene encoding it (AAB437493). The invention also encompasses variants of the hear resistant alkaline cellulase in which at least one amino acid residue is deleted, replaced or inserted. The Bacillus sp. KSM-S237 heat resistant alkaline cellulase gene was isolated using the Bacillus sp. No. 1139 alkaline cellulase gene derived PCR primers AAB37494-A97495. The Bacillus sp. KSM-S237 heat resistant alkaline cellulase gene can be used for the forcamilated in detergent for cleaning applications. The present sequence represents the Bacillus sp. KSM-S237 heat resistant alkaline cellulase which can be formulated in detergent for cleaning applications. The present sequence Gaps ö Query Match 77.4%; Score 17.8; DB 3; Length 3189; Best Local Similarity 90.5%; Pred. No. 3e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0; Sequence 3189 BP; 1088 A; 476 C; 704 G; 921 T; 0 U; 0 Other; A heat resistant alkaline cellulase gene. Claim 3; Page 6-10; 10pp; Japanese. ä

Sporulation associated gene, deactivation, deletion, sporulation suppression, sigE, sigF; spoIIE, spoIISB, sigG, spoIVCB, spoIIIC, recombinant protein production, gene, ds. Bacillus sp. KSM-64 sporulation-associated gene #2, SEQ 7797/c ABZS7797 Btandard; DNA; 3332 16-APR-2003 (first entry) ABZ57797; RESULT 15 ABZ57797/c

Incation/Qualifiers
610. 3078
/\*tag= a
610. 696
/\*tag= b
697. 3075
/\*tag= c
/\*tag= c
/\*tag= c
/\*tag= c
/\*tag= c KSM-64. Bacillus sp. sig\_peptide 

WO200297064-A1

05-DEC-2002

28-MAY-2002; 2002WO-JP005151.

29-MAY-2001; 2001JP-00160520

(KAOS ) KAO CORP.

Ozaki K; Tohata M, Ozawa T, Sawada K, Endo K,

WPI; 2003-140463/13. P-PSDB; ABP58993.

Bacillus strain having genes associated with sporulation inactivated for use as hosts in more efficient production of recombinant proteins.

Disclosure; Page 20-25; 29pp; Japanese.

The invention relates to microorganisms (particularly Bacillus species)
in which one or more sporulation-associated genes active in the medium to
clatter stages of sporulation have been deactivated or deleted. Such genes
include the sigh, sigh spoils, spoils, sigh, spoilsd and spoiling genes
include the sigh, sigh spoils.

The invention also relates to the recombinant production of a protein
cusing the microorganism of the invention. As the microorganisms of the
invention are incapable of producing spores, recombinant protein
confuced energy loss, reduced consumption of culture medium, and increased
conformation is more efficient, with reduced formation of by-products,
creduced energy loss, reduced consumption of culture medium, and increased
conformation is more efficient, with reduced formation of by-products,
creduced energy loss, reduced consumption of culture medium, and increased
conformation is more efficient, with reduced formation of time than is currently
the case. The microorganisms can be used to recombinantly production can
be efficiently carried out over a longer period of time than is currently
the case. The microorganisms can be used to recombinantly product far,
creduced. Consumption of culture sequence represents a
conduction sequence is given in the sequence listing, but is not
continued to in the specification 

Sequence 3332 BP; 1143 A; 501 C; 723 G; 965 T; 0 U; 0 Other;

Gaps ö Query Match 77.4%; Score 17.8; DB 7; Length 3332; Best Local Similarity 90.5%; Pred. No. 3e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0;

1 TTAATCATATGCGTTTTTGGT 21

Search completed: May 26, 2004, 17:50:10 Job time : 167.244 secs

2705 TTAATCGTATACGTTTTTGGT 2685 ઠે d

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May 26, 2004, 15:22:28; Search time 178.526 Seconds (without alignments) 594.900 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	œ.	M M	м :		Acal5469 Prokaryot	Aas82555 DNA encod	Abz15842 Arabidops	Abl33397 Human imm	Aad58282 Human tum	Aad58281 Human tum	Continuation (4 of	Aad58279 Human tum	Aac36413 Arabidops	Continuation (3 of	Abal3700 Human ner	Abal9908 Human ner	Aba20194 Human ner	Aba20198 Human ner	Abal9910 Human ner	Aba20197 Human ner	Abal8947 Human ner	Aba20195 Human ner	Abal9911 Human ner
SUMMARIBS	ACD28591	ACD28590	ACD28587	ACD28586	ACA15469	AAS82555	ABZ15842	ABL33397	AAD58282	AAD58281	ADE11169 3	AAD58279	AAC36413	ABA92787 2	ABA13700	ABA19908	ABA20194	ABA20198	ABA19910	ABA20197	ABA18947	ABA20195	ABA19911
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24	25	26	27	c 28	7	m	31	32	c 33	m	35	m	ო	38	33	40	c 41	c 42	c 43	C 44	45

## ALIGNMENTS

E. coli Arsk binding oligonucleotide CHROMS1B. ACD28591 standard; DNA; 25 BP. (first entry) 10-0CT-2003 ACD28591; ACD28591

Arsk; arsenic resistance operon; biosensor; ss; arsenic Escherichia coli.

15-AUG-2002; 2002US-00222952. US2003096275-A1. 22-MAY-2003. 

20-AUG-2001; 2001US-0313714P. (LAIN/) LAING L G. Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a charge in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of a analyte in a sample, detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the areance resistance operon of B. Coll) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid

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Gaps

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Indels

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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte, (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein, and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, detecting the arsenic resistance operon of B. coll) protein comprising an main acid sequence that is at least 90% identical to amino acids 1.97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid sequence comprising oligonucleotides appearing as ACD28564-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligonucleotide which binds to a consistence of the analyte in a sample of consistence of analyte analyte analyte and an analyte of the consistence of the consist
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sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds to a chromosomally expressed ArsR protein and is used in the biosensor of
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                                                                                                                                                              Sequence 25 BP; 13 A; 3 C; 2 G; 7 T; 0 U; 0 Other;
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25, Conservative
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100.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to a chromosomally expressed ArsR protein and is used in the biosensor of
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Pred. No. 1.6;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          Arsk; arsenic resistance operon; biosensor; ss; arsenic.
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0; Mismatches
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ACD28586/c
ID ACD28586 standarů; DNA; 42
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Best Local Similarity
Matches 25; Conserv
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   Matches
                                                                                                                       RESULT 3
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ArsR; arsenic resistance operon; biosensor; ss; arsenic.
                  E. coli Arsk binding oligonucleotide CHROMLIT.
                                                       15-AUG-2002; 2002US-00222952
                                                              20-AUG-2001; 2001US-0313714P
           10-OCT-2003 (first entry)
                                                                                    WPI; 2003-576876/54.
                                                                     (LAIN/) LAING L G.
                                 Escherichia coli.
                                        US2003096275-A1
                                               22-MAY-2003.
                                                                             Laing LG;
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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specifically binds the analyte; (2) an isolated nucleic acid containing a specifically by the protein; and (3) a detection system that indicates a change in binding of the protein; and containing a containing and to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte and an ArsR (encoded by part of the arsenic resistance operon of B. coll) protein comprising an amino acid sequence that is at least 90% indentical to amino acids 1-97 of the ArsR sequence appearing as ABUG3440 binding to a nucleic acid sequence comprising or ligonucleotides appearing as ACD28584+ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligonucleotide which binds to a chromosomally expressed ArsR protein and is used in the biosenar of the New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample. Sequence 42 BP; 11 A; 8 C; 5 G; 18 T; 0 U; 0 Other; Claim 35; Page 15; 36pp; English invention

ö 100.0%; Score 25; DB 8; Length 42; 100.0%; Pred. No. 1.6; 0; Indels 0; Mismatches 1 TAAGTCAAAACATATATGACTTAA 25 25; Conservative Query Match Best Local Similarity

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TAAGTCAAAACATATATGACTTAA 18

ACA15469 standard; DNA; 401 BP. (revised) (first entry) 27-OCT-2003 19-JUN-2003 ACA15469;

Prokaryotic essential gene antisense oligonucleotide #3339.

Antisense; 85; prokaryotic essential gene; cell proliferation; drug design.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-WAR-2002; 2002US-0362699P.

(BLIT-) BLITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

WPI; 2003-029926/02.

New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

Claim 1; SEQ ID NO 3339; 1766pp; English

The invention relates to an isolated nucleic acid comprising any one of the first antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid conditions a promoter operably linked to the nucleic acid conditions a promoter operably linked to the nucleic acid conditions are conditions and propertied whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the conformation; (4) identifying a gene in an operan required for proliferation or the activity of agene in an operan required for cellular proliferation; (8) inhibits and activity of required for proliferation or that has an activity against a biological pathway in which a proliferation-required gene or its gene product is equipment of an organism acts; (9) manufacturing an antibiots; (10) profiling a compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism sis present in a culture or collection of a proliferation of an organism. The antisense nucleic acids required for proliferation of an organism. The antisense nucleic acids are useful for the callular proliferation in cells other candidate molecules for rational cradised for proliferation in cells other than S. aureus, S. typhimurium, cradised for proliferation in cells other than S. aureus, S. typhimurium, antisense sequences of the invention. Note: The sequence details of the invention of an organism of the properties are genenced to the properties of the invention. Note: The sequence of the invention of an organism of the invention of the properties of the invention of the properties of the invention of the properties of the invention of the condit

ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 27-OCT-2003 to standardise OS field) 

Sequence 401 BP; 113 A; 68 C; 101 G; 119 T; 0 U; 0 Other;

Gaps ö Match 100.0%; Score 25; DB 7; Length 401; Local Similarity 100.0%; Pred. No. 1.6; es 25; Conservative 0; Mismatches 0; Indels Best Loca Matches

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RESULT

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13-FEB-2002

AAS82555;

AAS82555/c ID AAS825

11-OCT-2001

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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transpenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.8%; Score 20.2; DB 6; Length 2000; 88.0%; Pred. No. 1.2e+02;
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                                                                                                                     Arabidopsis thaliana stress regulated gene SEQ ID NO 3647.
                                                                                                                                                                      Arabidopsis thaliana; plant; gene; stress; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 1370.
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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ID ABL33397 standard; DNA; 5641 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kreps J, Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2001; 2001WO-US026685.
                                                                     21-JAN-2003 (first entry)
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                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-304127/34.
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les 22; Conserv
                                                                                                                                                                                                                                                                         WO200216655-A2.
                                                                                                                                                                                                                                                                                                                            28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harper JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL33397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of pulypeptide and polymucleotide sequences have applications in diagnostics, foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and and not appear in the printed specification, but was obtained in clear of the invention. Note: The sequence data for this classification, but was obtained in the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                           Human, chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2182 BP; 516 A; 569 C; 582 G; 515 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                           novel human diagnostic protein #18359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 18359; 103pp; English.
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                          AAS82555 standard; cDNA; 2182 BP.
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AB215842
ID AB215842 standard; DNA; 2000 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                             (first entry)
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nes 25; Conservative
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P-PSDB; ABG18368.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
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Gaps

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Indels

Query Match

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The invention relates to novel tumour suppressor gene, referred to as Lmt. The invention also relates to the field of cancer therapy and cancer diagnostics. The nucleic acid molecule is useful for screening a subject for the presence of an aberration in a gene encoding an LMT. The present sequence is human Lmt intron 3 DNA.
                                                                                                                                                                                                                                           Seguence 62782 BP; 15441 A; 9614 C; 9374 G; 14439 T; 0 U; 13914 Other;
             New nucleic acid molecule, useful for screening a subject for the presence of an aberration in a gene encoding an LMT.
                                                                                                                                                                                                                                                                                 Query Match 79.2%; Score 19.8; DB 8; Length 62782; Best Local Similarity 91.3%; Pred. No. 1.9e+02; Matches 21; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour suppressor gene, Lmt intron 2 DNA
                                                                             Claim 10; Page 333-358; 373pp; English
                                                                                                                                                                                                                                                                                                                                                                                              28437 ATGTCATAAACATATATGACTTA 28459
                                                                                                                                                                                                                                                                                                                                                                        2 AAGTCAAAACATATATGACTTA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD58281 standard; DNA; 62782 BP
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$££$2$8$86888$8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid rebuxemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, and inflammatoriy ucurofibromatosis, rheumatoic arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                    for
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful the diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.8%; Score 20.2; DB 6; Length 5641; Best Local Similarity 88.0%; Pred. No. 1.3e+02; Matches 22; Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1370; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                      02-JUL-2001; 2001WO-BP007537
                                                                                                                                                                                                                              30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                            (BPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17
                                                                                                      WO200200928-A2
                                                                Homo sapiens
                                                                                                                                              03-JAN-2002
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Gaps

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The invention relates to novel tumour suppressor gene, referred to as Imt. The invention also relates to the field of cancer therapy and cancer diagnostics. The nucleic acid molecule is useful for screening a subject for the presence of an aberration in a gene encoding an IMT. The present sequence is human Imt intron 2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other;
                                                                                                        Numour suppressor gene; Lant; cancer; therapy; cytostatic; human; ds
                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecule, useful for screening a subject for the presence of an aberration in a gene encoding an LMT.
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                                                                                                                                                                        WO2003066869-A1
                                                                                                                                           Homo sapiens
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Tumour suppressor gene; Lmt; cancer; therapy; cytostatic; human;

Human tumour suppressor gene, Lmt intron 3 DNA.

20-NOV-2003 (first entry)

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1536 ||| ||||||| |||||| |||||| 1512 1 TAAGTCAAAACATATATGACTTAA 25

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AAD58282 standard; DNA; 62782 BP.

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(HALL-) HALL INST MEDICAL RES WALTER & ELIZA

WPI; 2003-646311/61

Cook WD,

07-PEB-2003; 2003WO-AU000126.

WO2003066869-A1.

Homo sapiens

07-FEB-2002; 2002AU-00000371

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us-10-676-299-10.rng

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                             Arabidopsis thaliana DNA fragment SEQ ID NO: 13710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0134218P-99US-0134219P-99US-0134219P-99US-0134770P-99US-0134770R-99US-0135124P-99US-0135122P-99US-013522P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0137724P-99US-0138447P-99US-01394119P-99US-01394119P-99US-01394119P-
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990S-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126785P.
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990S-0139492P.
99US-0139454P.
99US-0139455P.
99US-0139456F.
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99US-0130449P.
99US-0130510P.
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99US-0139459P.
99US-0139460P.
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                                17-0CT-2000 (first entry)
                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                  EP1033405-A2.
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21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
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08-APR-1999;
16-APR-1999;
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27-MAY-1999;
28-MAY-1999;
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21-MAY-1999
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10-JUN-1999
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   AAC36413;
   ADE11169 from base 300001 (Human transporter protein encoding fragments LOCUS ADE11169 Accession Ade11169 Begin End
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 226475 BP; 61024 A; 41761 C; 40916 G; 57494 T; 0 U; 25280 Other;
                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour suppressor gene; Lmt; cancer; therapy; cytostatic; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule, useful for ecreening a subject for the presence of an aberration in a gene encoding an LMT.
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                                                                                                                                                   Score 19.8; DB 9; Length 94191;
Pred. No. 1.9e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour suppressor gene, Lmt reverse complement DNA.
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210000
310000
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AAC36413/c
ID AAC36413 standard; DNA; 1293 BP.
XX
                                                                                                                                                 Query Match
Best Local Similarity 91.3%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002; 2002AU-00000371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2003; 2003WO-AU000126
                                                                                    100001
200001
300001
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                             4.
            ADE111693
Continuation (4 of 4) of
WP Sequence split into 4
WP ADE11169 0
WP ADE11169 1
WP ADE11169 1
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                                                       Fragment Name
ADE11169 0
ADE11169 1
ADE11169 2
ADE11169 3
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RESULT 11
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99015-0145088P
99015-0147303P
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99015-0147303P
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18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
23-JUN-1999;
24-JUN-1999;
28-JUN-1999;
29-JUN-1999;
01-JUL-1999;
01-JUL-1999;
06-JUL-1999;
06-JUL-1999;
06-JUL-1999;
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22 - JUL - 1999;
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990S-0150884P

990S-0151065P

990S-0151060P

990S-0151303P

990S-0151303P

990S-015373P

990S-015373P

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990S-015473P

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990S-015563P

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1 Similarity 87.5%;
21; Conservative 1
26-AUG-1999

27-AUG-1999

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27-AUG-1999

10-SEP-1999

11-SEP-1999

11-SEP-1999

12-SEP-1999

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16-SEP-1999

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Gaps

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from base 200001 (Buchnera sp. genomic DNA SEQ ID is LOCUS AEA92787 Accession Aba92787
110000
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310000
410000
510000
610000 from fragments Begin 7} of ABA92787 into 7 fragments 100001 200001 300001 400001 500001 RESULT 14
ABA92787 2
Continuation (3 of 7) of
WP Sequence split into 7
WP ABA92787 0
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WP ABA92787 1
WP ABA92787 2
WP ABA92787 4
WP ABA92787 4
WP ABA92787 4

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Thu May 27 10:11:37 2004
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us-10-676-299-10.rng

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01-SEP-2000; 2000US-022944P.
01-SEP-2000; 2000US-022944P.
01-SEP-2000; 2000US-022944P.
05-SEP-2000; 2000US-0229503P.
06-SEP-2000; 2000US-0229503P.
06-SEP-2000; 2000US-023943P.
06-SEP-2000; 2000US-023943P.
06-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231443P.
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08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023149P.
14-SEP-2000; 2000US-023149P.
13-CCT-2000; 2000US-023149P.
13-CCT-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antibugal; antiparastitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
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                                               Length 110000,
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                                                                                            2; Indels
                                               Score 18.8; DB 6;
Pred. No. 4.6e+02;
0; Mismatches 2;
                                                                                                                                       640681
                                                                                                                                                                                                                                                                                                            ABA13700 standard; cDNA; 561 BP
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24-FEB-2000; 2000US-018652BP.
24-FEB-2000; 2000US-018635GP.
02-MAR-2000; 2000US-018635GP.
15-MAR-2000; 2000US-018635GP.
16-MAR-2000; 2000US-0198074P.
17-MAR-2000; 2000US-0198074P.
19-MAY-2000; 2000US-0198074P.
19-MAY-2000; 2000US-020467P.
28-JUN-2000; 2000US-0214886P.
11-JUL-2000; 2000US-0214886P.
11-JUL-2000; 2000US-021489P.
11-JUL-2000; 2000US-021489P.
11-JUL-2000; 2000US-021489P.
11-JUL-2000; 2000US-021896P.
14-JUL-2000; 2000US-021896P.
14-JUC-2000; 2000US-0228968P.
14-JUC-2000; 2000US-0228968P.
14-JUC-2000; 2000US-022896P.
15-JUC-2000; 2000US-022896P.
15-JUC-2000; 2000US-022896P.
16-JUC-2000; 2000US-022896P.
18-JUC-2000; 2000US-022896P.
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                                               Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative
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ABA92787_6
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2707; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Barash SC, Ruben SM;
                                 17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024926FP.
17-NOV-2000; 2000US-024926FP.
17-NOV-2000; 2000US-024926FP.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025186P.
18-DEC-2000; 2000US-025186P.
18-DEC-2000; 2000US-025186P.
18-DEC-2000; 2000US-025186P.
18-DEC-2000; 2000US-025186P.
                                                                                                                                                                                                                                                                                            08-DEC-2000; 2000US-0251990P
11-DEC-2000; 2000US-0254097P
05-JAN-2001; 2001US-0259678P
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P-PSDB; ABB17374.
                       17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins C (ABB14678-ABB18001) useful for preventing, treating or ameliorating conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and overtain cencer and other cancers of the adrenal gland, bone, bore marrow, breast, gastrointestinal tract, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycocardial isohaemias; (d) wound healing infectious diseases such as mycocardial isohaemias; (d) wound healing infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of infections. Note: The sequence data for this patent did not form part of from WIPO at ftp.wipo.int/pub/published pot\_sequences

Sequence 561 BP; 217 A; 96 C; 84 G; 155 T; 0 U; 9 Other;

Gaps . 0 Query Match 74.4%; Score 18.6; DB 5; Length 561; Best Local Similarity 84.0%; Pred. No. 5.1e+02; Matches 21; Conservative 0; Mismatches 4; Indels C

8

Search completed: May 26, 2004, 17:50:16 Job time : 178.526 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

TTTT \* C - C C Z - Q / Q - C T - S D

nucleic search, using sw model OM nucleic

Run on:

May 26, 2004, 16:18:00; Search time 47.8205 Seconds (without alignments) 348.146 Million cell updates/sec

US-10-676-299-3 30

1 ttaatcatatgcgtttttggttatgtgttg 30 Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

1365418 Total number of hits satisfying chosen parameters:

682709 segs, 277475446 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents NA:\*

1. \c9T2\_6/\ptodata/2/\tina/5A\_COMB.seq:\*

2. \c9T2\_6/\ptodata/2/\tina/5B\_COMB.seq:\*

3. \c9T2\_6/\ptodata/2/\tina/6A\_COMB.seq:\*

4. \c9T2\_6/\ptodata/2/\tina/6B\_COMB.seq:\*

5. \c9T2\_6/\ptodata/2/\tina/6B\_COMB.seq:\*

6. \c9T2\_6/\ptodata/2/\tina/PCTUS\_COMB.seq:\*

6. \c9T2\_6/\ptodata/2/\tina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			ð			SUMMARIES	
Result No.	ult No.	Score	Query Match	Length	DB	ID	Description
   	7	20.6	68.7	459	4	US-09-328-352-300	Sequence 300, App
	7	20	66.7	9028	m	US-08-913-014A-9	6
	m	20	66.7	9058	4	US-09-653-285-9	ō
	4	19.4	64.7	2481	4	US-09-328-352-3389	33
U	ហ	19.4	64.7	640681	4	US-09-790-988-1	
	v	19.2	64.0	47	4	US-09-422-978-2280	
υ	7	18.8	62.7	2911	4	US-09-349-740A-16	16,
O	œ	18.8	62.7	4500	4	US-09-349-740A-1	₩
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υ	11	18.8	62.7	1830121	4	US-09-643-990A-1	7
	12	18.6	62.0	1442	4	US-09-227-357-119	119,
	13	18.4	61.3	267	IJ	US-09-107-532A-1957	Sequence 1957, Ap
	14	18.4	61.3	3001	d,	US-09-539-333D-178	Sequence 178, App
	15	18.4	61.3	19513	4	US-10-204-708-39	Sequence 39, Appl
U	16	18.2	60.7	1026	4	US-09-134-001C-1995	199
	17	18	60.0	8537	4	US-10-204-708-41	41,
	18	17.8	59.3	519	ጥ	US-09-134-000C-724	724,
	19	17.8	59.3	774	٣	US-08-221-767-1	1, 4
υ	20	17.8	59.3	891	43	US-09-134-000C-1587	12
	21	17.8	59.3	1062	-	US-08-426-169-6	ģ
	22	17.8	59.3	1062	ო	US-09-233-813-6	ý
	23	17.8	59.3	1062	Ŋ	PCT-US95-09470-6	ģ
υ	24	17.8	59.3	1448	4	US-09-976-594-371	371
υ	25	17.8	59.3	1794	4	US-09-601-198-67	67,
	26	17.8	59.3	2304	4	-60	426,
ပ	27	17.8	59.3	63588	4	US-09-873-404-3	3,

Sequence 9, Application US/08913014A
; Sequence 9, Application US/08913014A
; Sequence 9, Application US/08913014A
; Eatent No. 6235878
; GENERAL INFORMATION:
 APPLICANT: Nishi, Kazunori
 APPLICANT: Shintani, Yakushi
; TILLE OF INVENTION: NOVEL PAS LIGAND-LIKE PROTEIN, ITS
TILLE OF INVENTION: PRODUCTION AND USE
; VORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVIG G. Conlin, Esq.
 ADDRESSEE: DAVIG G. CONPERTS E. USHWAN, LLP
 ADDRESSEE: DASSECTE
 ADDRE

ò 윱 RESULT 2 US-08-913-014A-9

equence 36, Appl equence 3, Appli equence 17, Appli equence 12, Appli equence 12, Appli equence 12, Appli equence 272, Appli equence 138, Appli equence 1464, Appli equence 260, Appli equence 360, Appli equence 350, Appli equence 354, Appli	0
36, Appli 3, Appli 17, Appli 12, Appli 12, Appl 12, Appl 12, Appl 1519, Appl 1519, Appl 1519, Appl 260, App 260, App 353, Appli 354, Appli 354, Appli 354, Appli 354, Appli 354, Appli 355, Appli 355, Appli 3578, Appli 3578, Appli 3578, Appli 3578, Appli 3578, Appli 3578, Appli 3578, Appli	Gaps
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28 17.8 59.3 92407 4 US-09-596-002-36 29 17.8 59.3 202001 4 US-09-734-674-3 30 17.8 59.3 202001 4 US-09-734-674-3 31 17.6 58.7 4868 1 US-09-543-681A-17 32 17.6 58.7 4868 5 PCT-US9-11310-12 33 17.6 58.7 4868 5 PCT-US9-11310-12 34 17.4 58.0 1253 4 US-09-543-681A-172 35 17.4 58.0 1253 4 US-09-543-681A-1519 36 17.4 58.0 1253 4 US-09-543-681A-1519 37 17.4 58.0 1253 4 US-09-543-681A-1519 38 17.4 58.0 1253 4 US-09-543-681A-1519 39 17.4 58.0 1253 4 US-09-107-532A-1464 41 17.4 58.0 2800 4 US-09-18-930-260 42 17.4 58.0 2800 4 US-09-18-950-3 44 17.2 57.3 424 4 US-09-543-681A-778 45 17.2 57.3 615 4 US-09-543-681A-778 45 17.2 57.3 615 4 US-09-543-681A-778 45 17.2 57.3 615 4 US-09-543-681A-778 46 17.2 57.3 615 4 US-09-543-681A-778 47 17.2 57.3 615 4 US-09-543-681A-778 48 17.2 57.3 615 4 US-09-543-681A-778 49 17.2 57.3 615 4 US-09-543-681A-778 41 17.2 57.3 615 4 US-09-543-681A-778 42 17.2 57.3 615 4 US-09-543-681A-778 43 17.2 57.3 615 4 US-09-543-681A-778 44 17.2 57.3 615 4 US-09-543-681A-778 45 17.2 57.3 615 4 US-09-543-681A-778 46 17.2 57.3 615 4 US-09-543-681A-778 47 17.2 57.3 615 4 US-09-543-681A-778 48 17.2 57.3 615 4 US-09-543-681A-778 49 17.2 57.3 615 4 US-09-543-681A-778 40 17.4 580 0 100-543-681A-778 41 17.2 57.3 615 4 US-09-543-681A-778 41 17.2 57.3 615 4 US-09-543-681A-778 42 17.2 57.3 615 4 US-09-543-681A-778 43 17.2 57.3 615 4 US-09-543-681A-778 44 17.2 57.3 615 4 US-09-543-681A-778 45 17.2 57.3 615 4 US-09-543-681A-778 46 17.2 57.3 615 4 US-09-543-681A-778 47 17.2 57.3 615 4 US-09-543-681A-778 48 17.2 57.3 615 4 US-09-543-681A-778 49 17.2 57.3 615 4 US-09-543-681A-778 40 17.4 580 0 100-100-100-100-100-100-100-100-100-	ORGANISM: Acinetobacter baumannii 9-328-352-300 ery Match st Local Similarity 85.2%; Pre tches 23; Conservative 0;
28 17.8 59.3 92407 4 US-09-29 17.8 59.3 202001 4 US-09-29 17.8 59.3 202001 4 US-09-29 17.6 58.7 4868 1 US-09-32 17.6 58.7 4868 1 US-09-32 17.6 58.7 4868 5 PCT-US-08-29 17.4 58.0 58.7 4868 5 PCT-US-08-29 17.4 58.0 1253 4 US-09-29 17.2 57.3 482 4 US-09-29 17.2 57.3 482 4 US-09-29 17.2 57.3 482 4 US-09-29 17.2 57.3 615 4 US-09-29 17.2 57.3	_ \frac{\frac{1}{2}}{2} \frac{1}{2} \frac{1}{2}
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                   2 TAATCATATGCGTTTTTGGTTATGTGTT 29
                                                      TYPE: Nucleic acid
STRANBENESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-653-285-9
         INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 9058
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.1%;
Matches 23; Conservative
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Best Local Similarity 79.3
Matches 23, Conservative
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US-09-328-352-3389
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US-09-790-988-1/c
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APPLICANT: Nishi, Kazunori
Hikichi, Yukiko
Shintani, Yasushi
TITLE OF INVENTION: NOVEL PAS LIGAND-LIKE PROTEIN, ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENČE ADDRESS:
ADDRESSEE: David G. Conlin, Esq.
DIXE, BRONSTEIN, ROBERTS & USHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
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MEDLUM TYPE: Diskette

COMPUTER: IBM Compatible

CONFUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASESBQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/653,285

FILING DATE: 31-Aug-2000

CLASSIFYCATION AVARE: 08/913,014

FILING DATE: CURKNOWN>

APPLICATION NUMBER: 08/913,014

FILING DATE: CURKNOWN>

APPLICATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 342/47694

TELEPRENCE/DOCKET NUMBER: 342/47694

TELEPRANCE 17-523-5440

TELEFRANCE COMMINOWN>
SOFTWARE: FastSRQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FLING DATE: 04-SEP-1997
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02/1997/02480
FILING DATE: July 17, 1997
ATTORNEY-AGBWT INFORMATION:
NAME: DAVIG G. Conlin
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 342/47694
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB:
Pred. No. 23;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.1%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
MOLECULE TYPE: genomic DNA
US-08-913-014A-9
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                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9058
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston, STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-09-653-285-9
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Sequence 3389, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICAMT: Gary L. Breton et al.
APPLICAMT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 3389
ILENGTH: 2481
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Sequence 1, Application US/09790988

Sequence 1, Application US/09790988

GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEAL
APPLICANT: HATCHI, MASAHIRA
APPLICANT: SARKAL, YOSHIYUKI
TITLE OF INVENTICN: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILLE REPRENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT APPLICATION NUMBER: US/09/790,988
PRIOR APPLICATION NUMBER: US/09/790,988
PRIOR PILING DATE: 2001-02-23
PRIOR PILING DATE: 2001-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PACENTIN VET: 2.1
SEQ ID NO 1
SEQ ID NO 1
SED INGTH: 640681
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Pred. No. 66;
0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 79.3%; Pred. No. 34;
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Acinetobacter baumannii
US-09-328-352-3389
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## APPLICANT: Liagace, Robert, B.
| APPLICANT: Liagace, Robert, B.
| APPLICANT: Patterson, Chandra |
| APPLICANT: Berg, Kim, L. |
| TILE OF INVENTION: NUCLEOTIDE SEQUENCES OF WORAXELLA CATARHALIS GENOME |
| FILE REFERENCE: PM-0008-4 US |
| CURRENT APPLICATION NUMBER: US/09/596,002 |
| CURRENT APPLICATION NUMBER: US/09/16 |
| PRIOR PILING DATE: 1099-06-16 |
| NUMBER OF SEQ ID NOS: 41 |
| SOFTWARE: PERL PROGRAM |
| SOFTWARE: PERL PROGRAM |
| SOFTWARE: PERL PROGRAM |
| SEQ ID NO 41 |
| LINGTH: 269223 |
| TYPE: DNA ORGANISM: Moraxella catarrhalis |
| FRATURE:
                                                                                                                                 Gaps
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                                                                             DB 4; Length 2911;
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                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Mascarenhas, Joseph P.
APPLICANT: He, Caiping
TILE REFERENCE: 0794.009A
CURRENT PELLON: NUMBER: US/09/349,740A
CURRENT PILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/092,277
PRIOR PILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: WordPerfect 8.0
SEQ ID NO 1
                                                                                                                                 ;
                                                                                                                                                                                                                                  2051 Treadeatatedeaatraderretreire 2022
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1 Similarity 76.7%; Pred. No. 64;
23; Conservative 0; Mismatches
                                                                          Query Match 62.7%; Score 18.8; E
Best Local Similarity 76.7%; Pred. No. 61;
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTACATOR AT A MANAGE CHARLES OF CANALOR AND A MANAGE CASTON: (450)

COTHER INFORMATION: n may be C,G,T or A MANAGEY: allele

COCHION: (546)

MAME/KEY: allele

LOCATION: (737)

CTHER INFORMATION: n may be C,G,T or A CHER INFORMATION: n may be C,G,T or A CHER INFORMATION: n may be C,G,T or A US-09-349-740A-1
; OTHER INFORMATION: n may be C,G,T or A US-09-349-740A-16
                                                                                                                                                                                                                                                                                                                                               US-09-349-740A-1/c
, Sequence 1, Application US/09349740A
; Patent No. 6476297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-596-002-41/c
; Sequence 41, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4500
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Best Local
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                                                                                                                                   US-09-422-978-2280

Sequence 2280, Application US/09422978

Sequence 2280, Application US/09422978

Patent No. 6537751

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

APPLICANT: Chumakov, Ilya

TILLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REPERENCS: GENSET.020C21

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT PILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER PILING DATE: 1998-04-21

EARLIER PILING DATE: 1998-04-21

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EARLIER FILING DATE: 1998-04-21

EARLIER PILING DATE: 1998-04-21
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CCATION: 24

COTHEN INFORMATION: 99-10146-202 : polymorphic base T or A

US-09-422-978-2280
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APPLICANT: He Caiping,
TITLE OF INVENTION: Melosis-Related Gene and Promoter:
FILE REFERENCE: 0794.009A,
CURRENT APPLICATION NUMBER: US/09/349,740A,
CURRENT ILING DATE: 1999-07-08
FRICH APPLICATION NUMBER: 60/092,277
FRICH APPLICATION NUMBER: 60/092,277
STOR FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: WordPerfect 8.0
SEQ ID NO 16
                                                   516370 Tradradicrandritricgiranardri 516342
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Pred. No. 25;
1; Mismatches
5
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LOCATION: (546)
OTHER INFORMATION: n may be C,G,T or A
NAME/KEY: allele
LOCATION: (737)
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Sequence 16, Application US/09349740A

; Patent No. 6476291

; GENERAL INFORMATION;
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MAME/KEY: allele
LOCATION: (450)
OTHER INFORMATION: n may be C,G,T
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ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.0%;
ilarity 80.8%;
Conservative
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Best Local Similarity
Matches 21; Conserv
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APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
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US-09-557-884-1/c

j Sequence 1, Application US/09557884

j Patent No. 6506581

GENERAL INFORMATION:

j APPLICANT: Pleischmann et al.

APPLICANT: Pleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of

Thereof, and Uses Thereof
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Pred. No. 1.18+02;
0; Mismatches 2; Indels 0; 0
                                                                                                              Length 269223;
                                                                                                                                                     ö
                                                                                                         Query Match 62.7%; Score 18.8; DB 4; Length 2
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.,
ZIP: 20850
COMPUTER READABLE FORM;
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OCRETATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
PILING DATE: 25-Apr-2000
CLASSIFICATION NUMBER: 08/476,102
PILING DATE: 15-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
PILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 41,971
REFERENCY DOCENTY NUMBER: PRISES
TELEPHONE: 301-309-8504
TTELEPHONE: 301-309-8439
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
  ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte template ID No. 6632636
; PUBLICATION INFORMATION;
US-09-596-A102-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESSEONDENCE ADDRESS:
ADDRESSEE: Huran Genome Sciences, Inc.
STREBT: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.7%; Scc...
90.9%; Pred. No. ...
0; Mismatches
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STRANDENESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                     142085 TTAATGATATGCGTTTTTGGCT 142064
                                                                                                                                                                                              22
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Best Local Similarity 90.9
Matches 20; Conservative
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RESULT 11
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Parent No. 6558289
GENERAL INFORMATION:

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HITLE OF INVENTION: The Nucleotide sequence of the sequence of
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ö Ö Gaps ö ö Length 1442; Indels Indels STREET: 100 CLTY
Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FLING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FLING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FLING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REPERENCE/POCKET NUMBER: GTC-012
TELERBHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 1957:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular 9 DB 4; DB 4; Query Match 62.0%; Score 18.6; Dest Local Similarity 84.0%; Pred. No. 67; Matches 21; Conservative 0; Mismatches Query Match 61.3%; Score 18.4; I Best Local Similarity 78.6%; Pred. No. 72; Matches 22; Conservative 0; Mismatches NAME/KEY: misc feature ; LOCATION: (B) LOCATION 1..567 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1957: US-09-107-532A-1957 3 AATCATAIGCGITTITGGTIAIGITG 30 ORGANISM: Enterococcus faecium 750 TAATCATATTGTTTATGGTTGTGT 774 2 TAATCATATGCGTTTTTGGTTATGT 26 TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHEFICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: 셤

RESULT 14

US-09-539-333D-178

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Sequence 39, Application US/10204708

Sequence 39, Application US/10204708

Sequence 39, Application US/10204708

Sequence 19, Application US/10204708

Sequence 19, Application US/10204708

Sequence 19, Application US/10204708

APPLICANT: PIERENBROCK, Christian

APPLICANT: PIERENBROCK, Christian

APPLICANT: PIERENBROCK, Christian

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: by Assessing DNA Methylation

TITLE OF INVENTION: by Assessing DNA Methylation

TITLE OF INVENTION: by Assessing DNA Methylation

CURRENT APPLICATION NUMBER: DS/10/204,708

CURRENT FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

LENGTH: 19513

TURN: DATE: DATE: 2000-09-01

LENGTH: 19513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
CTHER INFORMATION: chemically treated genomic DNA (Fomo sapiens)
US-10-204-708-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2843 TAATTATATATATATTATTGTTATTCTTTT 2870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TAATCATATGCGTTTTTGGTTATGTGTT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 22; Conservative
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       Sequence 178, Application US/0953933D

Patent No. 447208

CGNEGAL INFORMATION

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANTON NUMBER: US 60/132,065

PRIOR APPLICATION NUMBER: US 60/113,228

PRIOR APPLICATION NUMBER: US 60/145,915

PRIOR APPLICATION NUMBER: US 60/146,453

PRIOR PLING DATE: 1999-07-27

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: primer bind
LOCATION: 1665..1683
OTHER INPORMATION: downstream amplification primer, complement
FEATURE:
NAME/KEY: misc_binding
LOCATION: 1489..1513
OTHER INFORMATION: 99-15682-318 probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
61.3%; Score 18.4; DB 4; Length 3001;
Best Local Similarity 78.6%; Pred. No. 89;
Matches 22; Conservative 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: allele
NAME/KEY: 1501
OTHER INFORMATION: 99-15682-318 : polymorphic base A or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: cisc_binding
LOCATION: 1502..1521
OTHER INFORMATION: 99-15682-318.mis2, complement
PEATURE:
NAME/KEY: primer_bind
LOCATION: 1184..1202
OTHER INFORMATION: upstream amplification primer
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LOCKTION: 1482..1500
OTHER INFORMATION: 99-15682-318.misl
FRATURE:
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NAME/KEY: misc_feature

LOCATION: 1842

CHER INFORMATION: n=a, g, c or t
US-09-539-3330-178
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ORGANISM: Homo Sapiens
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Gaps

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us-10-676-299-3.rnpb

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RESULT 1
US-10-222-952A-3
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Sequence 7, Appli
Sequence 7, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 1085, Appl
Sequence 1085, Appli
Sequence 166036,
Sequence 119, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 19, Appl
                                                                                                                                                                 May 26, 2004, 17:50:29; Search time 615.897 Seconds (without alignments) 221.574 Million cell updates/sec
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1: /cgn2_6/prodata/2/pubpna/PcT_Raw PUB.esq:*
2: /cgn2_6/prodata/2/pubpna/PcT_Raw PUB.esq:*
3: /cgn2_6/prodata/2/pubpna/PcT_Raw PUB.esq:*
4: /cgn2_6/prodata/2/pubpna/USOG_NEW_PUB.seq:*
5: /cgn2_6/prodata/2/pubpna/USOG_NEW_PUB.seq:*
6: /cgn2_6/prodata/2/pubpna/USOG_NEW_PUB.seq:*
7: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
8: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
9: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
10: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
11: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
11: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
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12: /cgn2_6/prodata/2/pubpna/USIDB_PUBCOMB.seq:*
13: /cgn2_6/prodata/2/pubpna/USIDB_PUBCOMB.seq:*
14: /cgn2_6/prodata/2/pubpna/USIOB_NEW_PUB.seq:*
15: /cgn2_6/prodata/2/pubpna/USIOB_NEW_PUB.seq:*
16: /cgn2_6/prodata/2/pubpna/USIOB_NEW_PUB.seq:*
17: /cgn2_6/prodata/2/pubpna/USIOB_NEW_PUB.seq:*
18: /cgn2_6/prodata/2/pubpna/USIOB_NEW_PUB.seq:*
19: /cgn2_6/prodata/2/pubpna/USIOB_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-222-952A-4

3 US-10-222-952A-7

3 US-10-087-192-2014

5 US-10-087-192-412

1 US-08-867-701-10855

1 US-08-867-701-10855

5 US-10-222-952A-8

1 US-10-22-952A-8

1 US-10-22-952A
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30
1 ttaatcatatgcgtttttggttatgtgtg 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2960401 seqs, 2274450654 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                            nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                          Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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ស្រស្នេស្ត ស្នេស្ត្រស្ន
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e Match Length
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Seguence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                                       ನಿಟ್ಟಾ ೦೧:
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FRATURE:
7 OTHER INFORMATION: PLASLIT biotinylated top, long oligo sequence; biotinylated
7 OTHER INFORMATION: nucleotide at position 1
US-10-222-952A-3
                                                  Sequence 9, Appli
Sequence 50, Appl
Sequence 50, Appl
Sequence 1, Appl
Sequence 256, Appl
Sequence 256, Appl
Sequence 296689,
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Sequence 296689,
Sequence 296689,
Sequence 289306,
Sequence 289307,
Sequence 289307,
Sequence 289307,
Sequence 289307,
Sequence 289307,
Sequence 289306,
Sequence 289306,
Sequence 289306,
Sequence 119, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 1379, Appl
Sequence 1379, Appl
Sequence 1379, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 1379, Appl
Sequence 1379, Appl
Sequence 1373, Appl
Sequence 1375, Appl
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               Sequence Sequence Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/1022952A
; Sequence 3, Application US/1022952A
; Publication No. US20030096275A1
; GENERAL INFORMATION:
; APPLICANT: Regenesis
; APPLICANT: Laing, Lance
; TITLE OF INVENTION: BLOSENSOR FOR SMALL MOLECULE ANALYTES
; TITLE REFERENCE: 4107/11/443-US1
; CURRENT APPLICATION NUMBER: US/10/222,952A
; CURRENT FILING DATE: 2002-08-15
; PRIOR PILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 30; DB 15; Length 30; Best Local Similarity 100.0%; Pred. No. 0.052; Matches 30; Conservative 0; Mismatches 0; Indels
US-10-027-632-204483
US-10-027-632-204483
US-10-027-632-129002
US-10-027-632-129002
US-10-027-632-129002
US-10-221-144-501
US-10-231-58
US-10-175-523-58
US-10-175-523-61
US-10-175-523-61
US-10-175-523-61
US-10-240-453-256
US-10-027-632-29688
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US-10-027-632-29688
US-10-027-632-29688
US-10-027-632-29688
US-10-027-632-29688
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US-10-027-632-289306
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US-10-027-632-289306
US-10-027-632-289306
US-10-027-632-289306
US-10-027-632-289306
US-10-027-632-289306
US-10-246-485-11
US-10-240-485-11
US-10-240-485-11
US-10-21-613-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-10-222-952A-4/c
Sequence 4, Application US/10222952A
; Publication No. US20030096275Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
    66.7 520

66.7 684

66.7 34058

66.7 34058

66.0 251364

66.0 251364

66.0 251364

66.0 251364

67.0 251364

68.3 378361

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us-10-676-299-3.rnpb

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PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID MOS: 2059
SOFTWARE: PESECEQ for Windows Version 4.0
SEQ ID NO 2014
LENGTH: 248436
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
COGTANISM: Homo sapiens
COGTANISM: MOSCANISM: NAME/KEY: misc_feture
COGTANISM: 11...(248436)
COTTER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-10-087-192-412/c
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US-10-240-453-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: PLASSIT top, short biotinylated oligo sequence; biotinylated ) OTHER INFORMATION: nucleotide at position 1 US-10-222-952A-7
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                APPLICANT: Regenesis
APPLICANT: Regenesis
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REPRENCE: 4107/1144-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT PILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7. Application US/1022992A
; Sequence 7. Application US/1022992A
; Publication No. US20030096275A1
; CENERAL INFORMATION:
; APPLICANT: Regenesis
; APPLICANT: Laing, Lance
; TITLE OF INVERTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
; FILE REFERENCE: 4107/11443-US1
; CURRENT APPLICATION NUMBER: US/10/222,952A
; CURRENT FILING DATE: 2002-08-15
; PRIOR PRICATION NUMBER: US 60/313,714
; ROFTMARE: PARCHIL VERSION 3.1
; SSQ ID NOS: 13
; SSQ ID NOS: 13
; SBQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB 15; Length 28;
Pred. No. 0.29;
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21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: PLASLIB bottom, long oligo sequence
US-10-222-952A-4
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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
ITTLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR ITTLE OF INVENTION: CANCER
FILE REFERENCE: 52942200122
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                           93.3%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.7%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 21; Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AATCATATGCGTTTTTGGTTATGTTG 30
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                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 106.
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US-10-087-192-2014
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US-10-222-952A-7
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Matches
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Sequence 11, Application US/10240453
Sequence 11, Mapplication US/10240453
Publication No. US20030148326A1
Sequence 11, Mapplication No. US20030148326A1
Sequence 11, Mapplication No. US20030148326A1
SPUBLICANT: OLEK, Alexander
APPLICANT: BIRENBROCK, Christian
APPLICANT: BIRENBROCK, Christian
APPLICANT: BIRENBROCK, Christian
APPLICANT: BIRENBROCK, Christian
APPLICANT: BIRLIN, Murt
ITLE OF INVENTION: Diagnesis of Diseases Associated with DNA
ITLE OF INVENTION: With DNA TRANSCRIPTION
ITLE OF INVENTION: With DNA TRANSCRIPTION
FILE OF INVENTION: With DNA TRANSCRIPTION
FILE OF INVENTION: With DNA TRANSCRIPTION
FILE OF INVENTION: DIAGNES: 2002-10-02
FRIOR APPLICATION NUMBER: DE 10019173 8
FRIOR PILING DATE: 2000-04-06
FRIOR PILING DATE: 2000-04-06
FRIOR PILING DATE: 2000-04-06
FRIOR PILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-04-07
FRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
     Length 248436;
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Query Match 73.3%; Score 22; DB 13; Length 24 Best Local Similarity B3.3%; Pred. No. 2.6e+02; Matches 25; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                 76015 TTAATCATCTGTATTTGCTTATTTGTTG 76044
                                                                                                                                                                                                                    1 TTAATCATATGCGTTTTTGGTTATGTTG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Gaps

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Query Match 70.0%; Score 21; DB 15; Length 21; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 TAATCACATGAGTTTTTTTTGTTTTGTTTTG 275
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  PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF EDG ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LEVET IN 8
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        3 AATCATATGCGTTTTTGGTTA 23
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US-10-027-632-166036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10855, Application US/09867701
; Sequence 10855, Application US/09867701
; Patent No. US20020132237A1
; GANERAL INFORMATION:
; APPLICANT: Adjate, Paul A.; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TILLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; TILLE REPERBYCE: 210121.497
; CURRENT PAPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SEQ ID NO 10855
; LENGTH: 343
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Best Local Similarity 88.5%; Pred. No. 1.7e+02;
Matches 23; Conservative 0; Mismatches 3; Indels
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: $29452000122
CURRENT PELING DATE: 2002-03-01
FRIOR APPLICATION NUMBER: US 09/747,377
FRIOR APPLICATION NUMBER: US 09/747,377
FRIOR APPLICATION NUMBER: US 09/798,586
FRIOR FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: US 09/798,586
FRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 412
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Publication No. US20030096275A1
GENERAL INFORMATION:
APPLICANT: Regeneesis
APPLICANT: Ading, Lance
TITLE OF INVENTION: BIOSENSOR FOR SWALL WOLECULE ANALYTES
FILE REFERENCE: 4107/1L443-US1
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65299 ACTCATATGCTTTTTTGGGTATGAGTTG 65272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AATCATATGCGTTTTTGGTTATGTGTG 30
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NAME/KEY: misc_feature

NAME/CATION: (1)...(79860)

OTHER INFORMATION: n = A,T,C or G
US-10-087-192-412
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
US-09-867-701-10855
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US-09-867-701-10855
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US-10-222-952A-8/c
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US-10-027-623-166036/
US-10-027-623-166036, Application US/10027632
| Sequence 166036, Application US/10027632
| Publication No. US20030204075A9
| GENERAL INFORMATION:
| APPLICATION:
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| FILE REPERENCE: 108827.128
| CURRENT APPLICATION NUMBER: US/10/027,632
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US-10-221-714A-119
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Sequence 119, Application US/1021714A

Publication No. US20040046254A1

GENERAL INCORMATION:
APPLICANT: OLEX, Alexander
APPLICANT: PIEPEMBROCK, Christian
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE SERERENT SOURCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2001-03-15
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173,8
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173,8
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 119
LENGTH: 6022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 741;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 16;
Pred. No. 2.3e+02;
0; Mismatches 5
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 60/199,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PRILING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR PRIOR PRILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
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Best Local Similarity 82.8%;
Matches 24; Conservative
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US-10-027-632-166036
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US-10-221-714A-119
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1 TTAATCATAIGCGTTTTTGGTTATGTGTTG 30

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Sequence 1045, Application US/10311455
Fublication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION WIMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
FRIOR PELICATION NUMBER: DE 10032529.7
FRIOR PELING DATE: 2000-06-30
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1045
LENTH: 6022
Sequence 79, Application US/10239676;
Publication No. US2030082609A1
FERENCE INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEFENBROCK, Christian
APPLICANT: PIEFENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REPRENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT PILLING DATE: 2002-09-24
FRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 1001913.8
DE 1001913.8
DE 10019259.7
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
(S-10-239-676-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 24; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.4; DB 15;
Pred. No. 5.5e+02;
0; Mismatches 6;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.0%;
Matches 24; Conservative
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NUMBER OF SEQ ID NOS: 228
SEQ ID NO 79
LENGTH: 6022
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                                   NUMBER OF SEQ ID NOS: 325720
SOFTHRRE: FastSEQ for Windows Version 4.0
SEQ ID NO 204443
LENGTH: 520
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PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
US-10-027-632-204483
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                                                                                                                                                                                                                                                                                                    Sequence 85. Application US/10240453
| Sequence 85. Application US/10240453|
| Publication No. US2003014832641
| GENERAL INPORMATION:
| GENERAL INPORMATION:
| APPLICANT: DEFENING KOTK, Christian
| APPLICANT: DEFENING KOTK
| TITLE OF INVENTION: DAMESTORED OF Assessing the Methylation Status of Genes Associated
| TITLE OF INVENTION: DAMESTORED OF Assessing the Methylation Status of Genes Associated
| TITLE OF INVENTION: DAMESTORED OF ASSOCIATION OF ASSOC
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Publication No. US20020198371A1

JEGENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

FRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-44

PRIOR FILING DATE: 1000-02-44

PRIOR FILING DATE: 1000-02-44

PRIOR FILING DATE: 1000-02-44

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 24; Conservative 0; Mismatches 6;
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ORGANISM: Artificial Sequence
FEATURE:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic Run on:

May 26, 2004, 15:22:28; Search time 214.231 Seconds (without alignments) 594.900 Million cell updates/sec

US-10-676-299-3. 30 1 traatcatatgcgtttttggttatgtgtg 30

Title: Perfect score: Seguence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_29Jan04:\*

1: geneseq11980s:\*

2: geneseq11990s:\*

4: geneseq12001s:\*

5: geneseq12001s:\*

6: geneseq12001s:\*

7: geneseq12001s:\*

8: geneseq12003s:\*

9: geneseq12003s:\*

10: geneseq12003s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Q. I	Acd28584 E.	Acd28585 E. coli A	Acd28588 E. coli A	Abk28137 DNA trans	Aaa81455 N. mening	Continuation (15 o	Continuation (14 o	Aaf21610 Neisseria		Acd28589 E. coli A	Ada29013 DNA encod	Abl16815 Drosophil	Aaf56298 IS2 eleme	Aas45374 Chemicall	Aas46397 Tumour su	S	Abk28211 DNA trans	_	Abk37763 DNA seque	Aba02964 Human rib	Aav10663 Mouse Fas		Aal49583 Murine tu
Transpoor of the second	61	ACD28584	ACD28585	ACD28588	ABK28137	AAA81455	AAA81490 14	AAA81490 13	AAF21610	ABL87877	ACD28589	ADA29013	ABL16815	AAF56298	AAS45374	AAS46397	ABL33072	ABK28211	AAF91383	ABK37763	ABA02964	AAV10663	AAC87652	AAL49583
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	Score	30	28	23	21.6	21.6	21.6	21.6	21.6	21.2	21	20.6	20.4	20.4	20.4	20.4	20.4	20.4	20	20	20	20	20	20
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ABQ75766 AAS46774 AAZ67933 ADB49481	AAQ67726 ABK28382 AAL52246_1 AAC17853_	ABQ42337 ABQ42336 AAH52751 ADA32102	AAH54693 AAH54720 ADA53054 ABL32346 ABL34458	ABL54314 ABX31504 ABL70475 AAS61438 ABL33406
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## ALIGNMENTS

ACD28584 standard; DNA; 30 RESULT 1 ACD28584

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ACD28584;

entry) 10-OCT-2003

E. coli Arsk binding oligonucleotide PLASLIT. 

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003.

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

(LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated uncleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the arsenic resistance operon of E. coll) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid

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sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyre in a sample. The present sequence is the top strand of an oligonucleotide which binds to plasmid expressed Arsk protein and is used in the biosensor of the
                                                                                                                                                                                                                                             invention
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Seguence 30 BP; 5 A; 2 C; 7 G; 16 T; 0 U; 0 Other;

88888888

Query Match

100.0%; Score 30; DB 8; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 30; Conservative 0; Mismatches 0; Indels

1 TTAATCATATGCGTTTTTGGTTATGTTG 30

à g

TTAATCATATGCGTTTTTGGTFATGTGTTG 30

RESULT

ACD28585/c ID ACD28585 standard; DNA; 28

ACD28585;

entry) (first 10-OCT-2003

E. coli ArsR binding oligonucleotide PLASLIB.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003.

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

(LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte, (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and are a resence of an analyte in a sample, and are a sample to part of the arsenic resistance operon of E. coli) protein comprising an amino acid sequence appearing as Au63440 binding to a nucleic acid sequence appearing as Au63440 binding to a nucleic acid sequence appearing the presence of analyte in a sample. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligomuleoride which binds to be a plasmid expressed ArsR protein and is used in the biosensor of the 

Sequence 28 BP; 14 A; 7 C; 2 G; 5 T; 0 U; 0 Other;

93.3%; Score 28; DB 8; Length 28; 100.0%; Pred. No. 0.15; Best Local Similarity Query Match

30 28 AATCATATGCGTTTTTGGTTATGTTTG 1 3 AATCATATGCGTTTTTGGTTATGTTG 셤 Š

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Mismatches

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28; Conservative

Matches

KESULT 3 ACD28588 RESULT

ACD28588 Btandard; DNA; 23 BP.

ACD28588;

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10-OCT-2003 (first entry)

E. coli Arsk binding oligonucleotide PLASSIT.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli

US2003096275-A1

22-MAY-2003

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P

(LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specifical binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein of the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of the analyte in a sample, detecting the presence of an analyte in a sample, and an acid sequence chat is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABG6340 binding to a nucleic acid sequence appearing as ABG6340 binding to a nucleic acid sequence is the top strand of an oligonucleotide ABG894. The present sequence is the top strand of an oligonucleotide which binds to a plasmid expressed ArsR protein and is used in the biosensor of the 

Sequence 23 BP; 5 A; 2 C; 4 G; 12 T; 0 U; 0 Other;

Gaps ö DB 8; Length 23; 12; 0; Indels Local Similarity 100.0%; Fred. No. 12; les 23; Conservative 0; Mismatches 76.7%; Score 23; Query Match Matches

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23 rraarcararecerrrreerra 23 1 TTAATCATATGCGTTT

RESULT 4 ABK28137 ID ABK2

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ABK28137 standard; DNA; 6391

ABK28137 

(first entry) 23-APR-2002

DNA transcription associated genomic DNA #6.

DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA, cytosine methylation state; SNB; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezars syndrome; haematological disorder; tuberculosis; pramunological disorder; werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis neurodegenerative disorder; meurological disorder; erythropoiesis; neurodegenerative disorder; moradial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour.

WO200192565-A2

06-DEC-2001.

06-APR-2001; 2001WO-EP003973.

06-APR-2000; 2000DE-01019058. 07-APR-2000; 2000DE-01019173. 30-UTM-2000; 2000DE-01035529. 01-SEP-2000; 2000DE-01043826.

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2002-090046/12

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumors or cancer.

Claim 1; SEQ ID NO 11; 32pp; English.

The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of \$46 sequences, and an oligomer that hybridises to or is identical or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosting or tracting diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, themerchlogical disorders, immunological disorders, waardenburg neurological disorders, immunological disorders, waardenburg contraction, hypertension, angiogenesis, eythtropolesis, congenital heart disease, HDR syndrome, architis, polyglutamine disorders, solid tumours or cancer. Sequences ABX28127-ABX28472 represent DNA transcription associated genomic DNA molecules of the printed specification but was obtained in electronic format directly from the European Patent

Sequence 6391 BP; 1421 A; 156 C; 1688 G; 3126 T; 0 U; 0 Other;

ö Gaps .. DB 6; Length 6391; Indels 72.0%; Score 21.6; D 85.7%; Pred. No. 60; ive 0; Mismatches Best Local Similarity 85.7 Matches 24; Conservative Query Match

1000 TAATAATGIGIAFITIGGATATGIGIT 1027 2 TAATCATATGCGTTTTTGGTTATGTGTT

AAA81455/c

AAA81455 standard; DNA; 23532

AAA81455;

(first entry) 04-DEC-2000

N. meningitidis partial DNA sequence gnm\_3 SEQ ID NO:3.

Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.

Neisseria meningitidis.

WO200022430-A2.

20-APR-2000.

99WO-US023573. 08-OCT-1999; 98US-0103794P. 09-0CT-1998; 30-APR-1999;

(CHIR ) CHIRON CORP.

Tettelin H, Venter JC; Ratti G, Scarselli M, Scarlato V; Peterson J, C, Mora M, Frazer CM, Hickey E, Masignani V, Galeotti Rappuoli R, Pizza M;

WPI; 2000-318079/27.

Isolated nucleotide sequences of Neisseria meningitidis which can be in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea.

Claim 7; Page 253-260; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA8244 represent corresponding to the AA81250 to AAA81260 to AAA81263 to AAA81260 to AAA81263 and AAA812650 to AAA81265 represent Neisseria DNA sequences and their corresponding proteins; AAA8125 to AAA81259 and CAAA8124 trepresent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA8132 to AAA8125 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all cused in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the exemple, some of the manufacture of a medicament (or treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all corpus Meningococcus B cyanism-specific probes Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent corpusing neringenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins chart may be presumed targets for the immune system and which are not antigenic allocations. 

Sequence 23532 BP; 6919 A; 5186 C; 5000 G; 6427 T; 0 U; 0 Other;

variable regions

Query Match

DB 3; Length 23532; 72.0%; Score 21.6;

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The present invention describes the full length genome of Neisseria meningitidis B (NWB). The sequences in AAF21544 and AAF21607 to AAF21613 cepresent fragments of the NWB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (1.e. the last 49980 bp of AAF21541 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21547 is repeated at the beginning of AAF21609, and so on). AAF21545 to AAF21580 encode the Neisseria proteins or primers which are used in the exemplification of the present invention. The NWB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computer storage medium or computer databases can be used in a search to identify open reading frames (ORFS) or coding sequences within the NWB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the concept of the proteins which have more effective in vaccines than the concept on the proteins which are more effective in vaccines than the
                                                                                           Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis B full length genome sequence and open reading
frames are used to detect, treat and prevent Neisserial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 349980 BP; 86771 A; 92803 C; 86340 G; 84066 T; 0 U; 0 Other;
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Scarselli M,
                                                        Neisseria meningitidis B nucleotide sequence SEQ ID NO:111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tettelin H, , Ratti G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pizza M, Hickey E, Peterson J, Te
Masignani V, Galeotti C, Mora M,
Rappuoli R, Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Appendix A; 692pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL87877 standard; cDNA; 343 BP
                                                                                                                                                                                                                                                                                                                                30-APR-1999; 99US-0132068P-08-0CT-1999; 99WO-US023573.
28-FEB-2000; 2000GB-00004695.
                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US005928
                      13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) INST GENOMIC RES.
                                                                                                                                                                          Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-647603/62.
                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP
                                                                                                                                                                                                                  WO200066791-A1
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AAA81490 13/C
Continuation (14 of 15) of AAA81490 from base 1300001 (N. meningitidis B full length gen
NP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490
NP AAA81490 00 1 100001
NP AAA81490 00 1 100001 210000
NP AAA81490 01 200001 210000
NP AAA81490 05 200001 310000
NP AAA81490 05 500001 510000
NP AAA81490 06 500001 710000
NP AAA81490 06 500001 1010000
NP AAA81490 07 700001 810000
NP AAA81490 10 10100001 1110000
NP AAA81490 11 1100001 1210000
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LOCUS AAA81490 Accession Aaa81490
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                    4; Indels
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Pred. No. 67;
0; Mismatches
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Pred. No. 72;
0; Mismatches
                                                                                 18848 TAAIGATAIGCATTTAIGGTTATTIGIT 18821
Similarity 85.7%; Pred. No. 65; 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9388 TAATGATATGCATTTATGGTTATTTGTT 9361
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                                                          2 TAATCATATGCGTTTTTGGTTATGTGT 29
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710000
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1410000
1437668
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Continuation (15 of 15) of AAA81490 from P Sequence split into 15 fragments End WP Sequence split into 15 fragments End WP AAA81490 00 100001 210 WP AAA81490 03 200001 310 WP AAA81490 04 400001 310 WP AAA81490 05 600001 610 WP AAA81490 06 600001 610 WP AAA81490 09 800001 910 WP AAA81490 09 900001 1100 WP AAA81490 09 900001 1100 WP AAA81490 10 1000001 1210 WP AAA81490 10 1000001 1210 WP AAA81490 11 1100001 1210 WP AAA81490 11 11000001 1310 WP AAA81490 12 1200001 1433
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AAF21610/c
ID AAF21610 standard; DNA; 349980 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%;
llarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.0%;
larity 85.7%;
Conservative
  Best Local Similarity
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nes 24; Conser
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Matches
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Matches
                      Matches
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AAA81490_
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Scarlato V;

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Gaps

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Escherichia coli. US2003096275-A1.

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Human; ovarian cancer; ovarian tumour; cytostatic; gene;
             Human ovarian cancer related cDNA clone SEQ ID NO:10855
                                                             29-MAY-2001; 2001WO-US017756
                                                                     26-MAY-2000; 2000US-0207484P
    17-MAY-2002 (first entry)
                                                                               (CORI-) CORIXA CORP.
                                                                                                  WPI; 2002-122075/16.
                                         WO200192581-A2
                                Homo sapiens,
                                                                                                                          polypeptide
                                                   06-DEC-2001
                                                                                        Algate PA,
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Jones

Harlocker SL,

The present invention describes a composition (1) comprising: carriers and annual and a polypeptide (III) of a ovarian tumnour prolypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in AB177021 to AB187934, (III) encoding (III) having a sequence (S2), a T cell population of (III), or antigen presenting cells that express (III) (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably carryidising to (IV) and comparing the amount of polynucleotide hybridising to (IV) and comparing the amount of polynucleotide hybridising to (IV) is detected preferably by an and comparing the amount of polynucleotide hybridising to (IV) is detected preferably by useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells specific for an ovarian tumour protein comprising contacting T cells specific for an ovarian useful in design and preparation of fiboxyme molecules for inhibiting useful in design and preparation of fiboxyme molecules and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour colNNA Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing Claim 1; SEQ ID NO 10855; 489pp; English library using well known techniques

ô Gaps ö Query Match 70.7%; Score 21.2; DB 6; Length 343; Best Local Similarity 88.5%; Pred. No. 72; Matches 23; Conservative 0; Mismatches 3; Indels 0 Sequence 343 BP; 117 A; 52 C; 50 G; 124 T; 0 U; 0 Other;

TTAATCAGATGCCTTTTTAGTTATGT 103 1 TTAATCATATGCGTTTTTGGTTATGT 26

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ACD28589 standard; DNA; 21 ACD28589; 

E. coli ArsR binding oligonucleotide PLASSIB. (first entry)

10-OCT-2003

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specifically binds the analyte; (2) an isolated nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, are the arsenic resistance operon of B. coll) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as ABC63440 binding to a nucleic acid the Arsk sequence appearing the presence of analyte in a sample. The system is useful for detecting the presence of analyte in a sample. The speam is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds is a sample.
                                                                                                                                                                                                                                                                                                                                                   New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 35; Page 15; 36pp; English
                                                                                                                                              15-AUG-2002; 2002US-00222952
                                                                                                                                                                                       20-AUG-2001; 2001US-0313714P
                                                                                                                                                                                                                                                                                                                 WPI; 2003-576876/54.
                                                                                                                                                                                                                                                                                                                                                                                                                       analyte in a sample
                                                                                                                                                                                                                                  (LAIN/) LAING L G.
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Gaps ö 70.0%; Score 21; DB 8; Length 21; 100.0%; Pred. No. 73; 0; Indels iive 0; Mismatches 0; Indels Local Similarity 100. nes 21; Conservative Query Match Matches

Sequence 21 BP; 10 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

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3 AATCATATGCGTTTTTGGTTA 23 21 AATCATATGCGTTTTTTGGTTA 1 Š g

ADA29013 standard; DNA; 459 (first entry) 20-NOV-2003 ADA29013; RESULT 11 ADA29013 

BP.

DNA encoding Acinetobacter baumannii protein #300.

ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial; vaccine; plant biocontrol agent.

Acinetobacter baumannii

13-MAY-2003.

JS6562958-B1

99US-00328352 14-JUN-1999;

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                                                                                                                       New Acinetobacter baumanii proteins and mucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                   The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genomic polynucleotide SEQ ID NO 1918.
                                                                                                                                                                                                                                                                                                                                                                                     68.7%; Score 20.6; DB 8; Length 459; larity 85.2%; Pred. No. 1.38+02; Conservative 0; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1918; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                               Sequence 459 BP; 93 A; 90 C; 102 G; 174 T; 0 U; 0 Other;
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                                                                                                                                                                                            Example, SEQ ID NO 300; 328pp; English.
                          (GENO-) GENOME THERAPEUTICS CORP.
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11-JUL-2000; 2000US-00614150.
 98US-0088701P.
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Best Local Similarity
Matches 23; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
                                                                                2003-576092/54.
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                                                                                WPI; 2003-576092/
P-PSDB; ADA33139.
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 09-JUN-1998;
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                                                       Breton G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel miniature inverted-repeat transposable element (MITE)-like element useful for constructing transgene expression cassette for stably creating genetically engineered organisms capable of expression of transgene.
                           18
The invention relates to an isolated mucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                             Query Match 68.0%; Score 20.4; DB 4; Length 1137; Best Local Similarity 80.0%; Pred. No. 1.6e+02; Matches 24; Conservative 0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                         Sequence 1137 BP; 309 A; 239 C; 262 G; 327 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                   203 TTATACATATGCGTTTTGTGTTAAGTGCTG 232
                                                                                                                                                                                                                                                                                                                                            1 TTAATCATATGCGTTTTTGGTTATGTTG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1999; 99JP-00206316.
21-JUL-1999; 99JP-00206320.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IS2 element sequence #5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-147351/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200105986-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Daucus carota.
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Local Sim.
24;
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Matches
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us-10-676-299-3.rng

Cell cycle; human, CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds; Chemically pretreated genomic DNA associated with cell cycle #40. 331 TABATTATATGTGATTTTGATTATGTGTGG 360 Berlin K; 15-MAR-2000; 2000DE-01013847. 06-APR-2000; 2000DE-01019058. 07-APR-2000; 2000DE-01019173. 30-JUN-2000; 2000DE-01043826. AAS45374 standard; DNA; 6022 15-MAR-2001; 2001WO-EP002945 (first entry) Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-602751/68. WO200168911-A2 Homo sapiens. 18-DEC-2001 20-SEP-2001 PCR primer AAS45374; н Olek A, RESULT 14

A 24,5,374

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A 24,5,5,374

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A 24,5,5,5,5,5,5

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Designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle.

Claim 1; SEQ ID NO 79; 28pp; English.

Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for and/or epigenetic parameters, the differences serving as basis for The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers

Sequence 6022 BP; 1478 A; 252 C; 1512 G; 2780 T; 0 U; 0 Other;

ö Score 20.4; DB 4; Length 6022; Pred. No. 1.8e+02; 6; Indels 0; Mismatches 1 TTAATCATATGCGTTTTTGGTTATGTTG 30 68.0%; 80.08; 24; Conservative Local Similarity Query Match Matches ઠે

2072 TIAATGATATTATTTTTGGTTATGTAATG 2101

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Gaps

₽ AAS46397 standard; DNA; 6022 RESULT 15 AAS46397

AAS46397;

(first entry) 18-DEC-2001

Tumour suppressor gene derived chemically modified sequence #119.

Human; tumour; cytostatic; cancer; tumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.

Homo sapiens

#O200168912-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-EP002955.

15-MAR-2000, 2000DE-01013847. 06-APR-2000, 2000DE-01019056. 07-APR-2000, 2000DE-01019173. 30-JUN-2000, 2000DE-01043826. 01-SEP-2000, 2000DE-01043826.

(EPIG-) EPIGENOMICS AG

Berlin K; Dlek A, Piepenbrock C,

WPI; 2001-602752/68

Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.

Claim 1; SEQ ID NO 119; 27pp; English

The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid—oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single culleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or proposition to specific diseases, by analysing chiseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of cytosine methylations. The parameters may be compared to another set of partients and/or epigenetic parameters may be compared to another set of partients. The present sequence is one of the 533 genomic sequences can enter the form the parameters and oncogenes. Note: The sequence data for this patent did not form at of the printed specification, but was obtained in electronic form at diseases. ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 6022 BP; 1478 A; 252 C; 1512 G; 2780 T; 0 U; 0 Other;

68.0%; Score 20.4; DB 4; Length 6022; 80.0%; Pred. No. 1.8e+02; ive 0; Mismatches 6; Indels 0; Local Similarity 80.0%; les 24; Conservative Query Match Best Loc Matches

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1 TTAATCATATGCGTTTTTGGTTATGTTG 30

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Search completed: May 26, 2004, 17:49:59 Job time : 219.231 secs

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May 26, 2004, 16:21:09 ; Search time 2078.59 Seconds (without alignments) 430.997 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		BG845098 1024008G0	BH370025 AG-ND-170	CD845514 RF02,143J	BH376658 AG-ND-171
SUMMARIES			ΩI		BG845098	BH370025	CD845514	BH376658
			8		75	28	17	78
			Match Length DB ID		677	400	695	814
	40	Query	Match	1 1 1 1 1 1 1	77.3	73.3	22 73.3	73.3
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AZ248907 RPCI-23-5 CD843195 RF02.130P BQ704555 BN01 02b0 AI738836 EX28JI.x BX111464 BX111464 BH193131 TC3-73D19 BF813601 MR2-CI018 BB186053 BB186053	2 PCSC202 1 PCSC187 0 PCSC187 6 f180h07 6 f180h07 f158a09 fd16e03		40 MUS	RPCI-2 EST317 RPCI-2 LP04121 CH240 034 0
AZ248907 CD843195 BQ704555 AI738836 AI738836 BX111464 BK193131 BF813601 BB186053	CA907972 CA907971 CA907970 B1878636 BM156934 A1666913 AW344027		AKU4374 BM16458 BH9898 CG91999 CNS017R AV228225 BG58611 BZ084528	<b>«</b>
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## **ALIGNMENTS**

	BG845098 677 bp mRNA linear EST 29-MAY-2001		Chlamydomonas reinhardtii cDNA, mRNA sequence.		BG845098.1 GI:14226282	BST.	Chlamydomonas reinhardtii	M Chlamydomonas reinhardtii	Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;	Chlamydomonadaceae; Chlamydomonas.			McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.	Analyses of the Chlamydomonas reinhardtii Genome: A Model,	Unicellular System for Analyzing Gene Function and Regulation in	Vascular Plants; project phase 2		Contact: Charles Hauser	DCMB Box 91000	Duke University	Durham, NC 27708-1000	Tel: 919 613 8159	Fax: 919 613 8177	Email: chauser@duke.edu.	Location/Qualifiers	
RESULT 1 BG845098	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REPERENCE	AUTHORS		TITLE			JOURNAL	COMMENT							FEATURES	

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CDB45514.1 GI:32529336
BST.
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Matches 25; Conservative
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                                                                                                                                                                            /note="Vector: pBluescript II SK-, Site_I: EcoRI; Site_2: Aholf This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in the ambient levels of CC2 and HS medium bubbled with 5½ CO2 PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5′) and XhoI (3′) sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6; 791-806."
1. .677
/organism="Chlamydomonas reinhardtii"
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db xref="taxon:3055"
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AG-ND-170H24.TR ND-TAM Anopheles gambiae genomic clone
AG-ND-170H24, genomic survey sequence.
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This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
the minimize the inclusion of DNA from micrororganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&W Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
Seq primer: MI3 Rev
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1 (bases 1 to 400)

Hong Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,

Ren, C., Huff, B.R., Carlile, J.L., Black, K., Zhang, H.-B.,

Gardmer, M.J. and Collins, F.H.

Construction of a BAC library and generation of BAC end

sequence-tagged connectors for genome sequencing of the African

malaria mosquito Anopheles gambiae

Mol. Genet. Genomics 268 (6), 720-728 (2003)
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Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.3%; Score 23.2; DB 12; Length 677; llarity 89.3%; Pred. No. 4.6e+02; Conservative 0; Mismatches 3; Indels 0;
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 AGTCATATGCGTCTTTTGTTATGTGTTG 487
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BH376658
AG-ND-171113.TR ND-TAM Anopheles gambiae genomic clone
AG-ND-171113, genomic survey sequence.
BH376658
BH376658.1 GI:17322800
GSS.
Anopheles gambiae (African malaria mosquito)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD845514 692 695 bp mRNA linear EST 11-JUL-2003 RFO2.143J06F011228 RFO2 Brassica napus cDNA clone RFO2143J06, mRNA sequence.
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Brassica napus
Brassica napus
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Fracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 695)
Genoplante.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
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Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Flas sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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/db xref="texon.7165"
/clone="AG-ND-170H24"
/clone llb="ND-TRA"
/note="Vector: pECBAC1; Site_1: HindIII"
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Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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/clone="RRO2143306"
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Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 928
Fax: 301 838 928
Fax: 301 838 928
Fax: 301 838 928
Fax: John and sequenced by The Institute for Genomic Research
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microaganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
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Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinzet, B., Levins, M., Mcgann, S., Tseegaye, G., Geer, K., Krol, M., de Mouse BAC End Sequences from Library RPCI-23
Other GSSs: RPCI-23-57D7.TV
Contact: Shaying Zhao
                                                                          1 (bases 1 to 814)
Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
Ren, C., Huff, B.R., Carlile, J.L., Black, K., Zhang, H.-B.,
Gardner, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
malaria mosquito Anophales gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
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                        Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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/organa="Anopheles gambiae"
/mol type="genomic DNA"
/strain="pBST"
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/clone="AG-ND-171113"
/clone_lib="ND-TAM"
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Mus musculus
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Class: BAC ends.
  Anopheles gambiae
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
East 10 2088
Email: schaochigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieteradejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Generics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 57 row: D column: 7
Seq primer: 8P6
Class: BAC ends.
Location/Qualifiers
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// Jab host-"DH108
// Ja
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RFO2.130P04F011011 RFO2 Brassica napus cDNA clone RFO2130P04, mRNA
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Brassica napus
Brassica napus
Brassica napus
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Contact: Genoplante
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Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0;
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/mol type="mRNA"
/culTivar="samourai (restored line)"
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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clone="RPCI-23-57D7"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Parayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 337.
Ilcation/cloudifiers
Location/confidence
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/mol_type="mRNA"
/mol_type="mRNA"
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/dlone=TRMAGE:2219684"
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/tissue_type="tumor, 5 pooled (see description)"
/tissue_type="tumor, 5 pooled (see description)"
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/clone=lorgan: oravy; Vector: pcMV-SPORT6, Site_1: Sall;
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/site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
/Average insert size 1.35 kb. Tumor types include: mixed
/mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"
Allibear EST 18-JUN-1999
tr28911.x1 NCI_CGAP_Ov23 Homo sapiens CDNA clone IMAGE:2219684 3',
mRNA sequence.
                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 33. NCI-CGAP. http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AI738836.1 GI:5100817
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Homo sapiens
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/db xref="restar"
/db xref="restar"
/clone="Bn01 02b08"
/clone="Bn01 02b08"
/clone lib="Bn01 AAFC ECORC transgenic Brassica napus_over
/note="Vector: Bluescript SK+/Xhoi_EcoRi; Site 1:
/note="Vector: Bluescript SK+/Xhoi_EcoRi; Site 1:
/site 2: Xhoi; Germinated in soil flats and seedlings grown
for 3 weeks in a conviron B-15 cabinet set at 200C /16 hr
light (250 Bm-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
collected at 9 am and immediately frozen."
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Bn01_ARFC_ECORC_transgenic_Brassica_napus_overexpressing_BNCB517_co
nstitutively_frost_tolerant_Brassica_napus_cDNA_clone_Bn01_02b08,
mRNA_sequence.
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                                                                                                                                                                                                                        Score 21.6; DB 14; Length 666;
Pred. No. 1.6e+03;
0; Mismatches 6; Indels 0
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                           /db_xref="taxon:3708"
/clone="RF02130P04"
/tissue_type="anthers"
/clone_Tib="RF02"
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Location/Qualifiers
1. 154
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/cultivar="Westar"
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BQ704555.1 GI:21843974
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80.0%;
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Tel: (613) 759-1662
Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                                                                                            1 TTAATCATATGCGTTT
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Matches 23;
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ORIGIN

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BX111464 NCI CGAP Ov23 Homo sapiens cDNA clone IMACp998L215489 ;
IMAGE:2219684, mRNA sequence.
                                                                                                                                                                                                            Homo sapiens

By By Raryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Extheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 359)

1 (bases 1 to 359)

Babert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schreider, D. and Korn, B.

Human UnigeneSet - RZPD3

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld $80, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                             TITLE
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AUTHORS
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RESULT 8 AI738836

d 8

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Gaps

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Length 343; 3, Indels .. 0

Gaps

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/db xrefe="taxon:569" (done="TC3-7D19")
/clone="TC3-7D19" (done="T
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Fax: +55-11-2707001
Email: saimpson@ludwig.org.br
Email: saimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-CI0186-301100-007-b09&t23=2000-1130&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 93
High quality sequence stort: 70
According Homo sapiens"

//organiam=Homo sapiens"
//db xef="taxxon:5606"
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1 (bases 1 to 220)

Dias Neto, S., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Rodai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, i.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF813601 220 bp mRNA linear EST 12-JAN-2001
MR2-C10186-301100-007-b09 C10186 Homo sapiens cDNA, mRNA sequence.
BF813601
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|Coone_lib="Cloude"
|rocte="Organ: colon ins; Vector: puc18; Site 1: Sma1;
|site_2: Sma1; A mini-library was made by cloning products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORP expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Best Local Similarity 82.8%; Pred. No. 3.1e+03;
Matches 24; Conservative 0; Mismatches 5; Indels
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     type="genomic DNA"
                                        strain="CL Brener"
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Unpublished (2001)
Other_GSSe: CT3-73D19_TV
Contact: Bjorn Andersson
Department of Genetics and Pathology
Uppsala University
Rudbeck Laboratory, SE-751 85, Uppsala, Sweden
Tel: 46 18 471 4107
Fax: 46 18 471 4108
Fax: 46 18 471 4107
Fax: 47 4107
Fax: 46 18 471 4107
Fax: 46 18 471 4107
Fax: 46 18 471 4107
Fax: 47 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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                       RZPDIAB; ITANGENIAL TANGENIAL CONTROLLECTION;
RZPDIAB; ITANGENIAL CONTROLLE NO.972)
Human UnigeneSet - RZPD3 (RZPDIAB NO.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response7libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomiorschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 101
Fax: +49 30 32639 101
Fax: -49 50 62639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
Location/Qualifiers
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Bukaryota; Buglenozoa, Kinetoplastida, Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases i to 165)
Kluge, S., Edwards, R.B., Nilsson, D., Bontempi, E.J., Myler, P.,
Stuart, K., Ghedin, B., El-Sayed, N. A. and Andersson, B.
Clustering and analysis of BAC-end and GSS sequences from
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1. .165
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/organism="Homo sapiens"
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RZPD; IMAGD998L215489.
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/dev_stage="f-days post-pollination"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA907972
PCSC20237 Scarlet Runner Bean Suspensor Region TriplEx2 Phaseolus coccineus cDNA 5' similar to Actin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="spinal cord"
/dev stages=adnis.
/dev stages=adnis.
/dlone_lib="RIKEN full-length enriched, adult male spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Molecular, Cell, & Developmental Biology
University of California, Los Angeles
621 Charles B. Young Drive South, Los Angeles, CA 90095-1606, USA
721: 310 825 3270
Fax: 310 825 8201
Fax: 310 825 8201
Fax: 510 825 8201
Fax: 510 825 8201
Fourier: 5 TriplEx
POLYA-Yes.
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82.8%; Pred. No. 3e+03;
iive 0; Mismatches 5;
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    clone="A330031F19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002) Contact: Goldberg, R.B.
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Phaseolus coccineus
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CA907972
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AUTHORS
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RIXEM Mouse ESTS (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Bmail: genome-res@gsc.riken.go.jp,
URL:http://genome-res@gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermomactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,X., Izawa,M., Rawai,J.,
Okazaki,Y., carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
Highh-efficiency full-length CDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Butheria; Rodentia; Craniata; Vertebrata; Euteleostom;

Rummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 22)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Pukuda, S., Pukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Salto, H., Sakai, C., Salco, K.,
Shibata, Y., Suzuki, H., Tagawa, A.,
Takahashi, F., Tominaga, N., Toye, T., Tsunoda, Y., Matahiki, A.,
Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
Haysahizaki, Y.,
Haysahizaki, Y.,
Haysahizaki, Y.,
Haysahizaki, Y.,
Haysahizaki, Y.,

Kananaka, A., Yoshika, Y., Yoshino, M., Muramatsu, M. and
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - indwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                     BB186053 RIKEN full-length enriched, acult male spinal cord Mus musculus cDNA clone A330031F19 3', mRNA sequence.
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                                                                                                                                                           Length 220;
                                                                                                                                                                                                             5; Indels
                                                                                                                                                                Score 21; DB 10;
Pred. No. 3e+03;
                                                                                                                                               70.0%; Scor. No. 30. 82.0%; Pred. No. 30. 90. Mismatches
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BB186053.1 GI:8846624
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                                                                                                                                                                Query Match
Best Local Similarity
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JOURNAL
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BB186053
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Gaps ö

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/note="Organ: Suspensor Region of Globular-Stage Embryos, Vector: TriplEx2; Site_1: SfilA, Site_2: SfilB, Suspensor regions were micro-disgected from globular-stage embryos six days after pollination from greenhouse-grown plants [Weterings et al., Plant Cell 13, 2409-2425 (2001)]. Double-stranded CDNA was synthesized from suspensor mRNA using the SWART CDNA Library Construction Kit according to the manufacturer (Clontech). The suspensor cDNA fragments were directionally ligated into the Sil restriction site of the lambda TriplEx2 vector (Clontech), and the recombinant CDNAs were transformed into E. coli XLI-Blue cells (Clontech). Suspensor cDNA plasmids used for directional sequencing were obtained by in vivo excision from the lambda TriplEx2 recombinants in E. coli BM25.8
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/db xref="taxon:3886"
/dev_stage="6-days post-pollination"
/clone_lib="Scarlet Runner Bean Suspensor Region TriplEx2"
/clone_lib="Scarlet Runner Bean Suspensor Region TriplEx2"
/note="forgan: Suspensor Region of Globular-Stage Embryos:
/vector: TriplEx2; Site_1: SfilA; Site_2: SfilB; Suspensor regions were micro-dissected from globular-stage embryos six days after pollination from greenhouse-grown plants [weterings et al., Plant Cell 13, 2409-2425 (2001)].
Double-stranded cDNA was synthesized from suspensor mRNA using the SMART cDNA inbrary Construction Rit according to the manufacturer (Clontech). The suspensor cDNA fragments were directionally ligated into the Sfil restriction site
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Relroy, K.E., Choi, P.S., Harada, J.J., Fischer, R.L. and Goldberg, R.B.

Goldberg, R.B.

Goldberg, R.B.

Gene Activity in Different Regions of a Post-Fertilization Plant Embryo by EST Analysis

Unpublished (2002)

Contact: Goldberg, R.B.

Department of Molecular, Cell, & Developmental Biology
University of California, Los Angeles

G21 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA Tel: 310 825 8201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA907971

209 bp mRNA linear EST 27-DEC-2002 PCSC18727 Scarlet Runner Bean Suspensor Region TriplEx2 Phaseolus coccineus cDNA 5' similar to Actin, mRNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
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Pred. No. 2.8e+03;
0; Mismatches 5; Indels
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/mol_type="mRNA"
/cultivar="Hammond's Dwarf Scarlet"
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Seg primer: 5' TriplEx
POLYA=Yes.
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CA907971
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CA907970 430 bp mRNA linear EST 27-DEC-2002 PCS03468 Scarlet Runner Bean Suspensor Region TriplEx2 Phaseolus coccineus cDNA 5' similar to Actin, mRNA sequence.
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Phaseolus coccineus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Phaseoleae;
of the lambda TriplEx2 vector {Clontech}, and the recombinant cDNAs were transformed into B. coli XL1-Blue cells (Clontech). Suspensor cDNA plasmids used for directional sequencing were obtained by in vivo excision from the lambda TriplEx2 recombinants in B. coli BM25.8 cells (Clontech)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Activity in Different Regions of a Post-Fertilization Plant Embryo by Est Analysis
Unpublished (2002)
Unpublished (2002)
Contact: Goldberg, R.B.
Department of Molecular, Cell, & Developmental Biology
University of California, Los Angeles
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Tel: 310 825 8201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 430)
Bui,A., Le,B.H., Weterings,K., Bi,Y.-P., Choi,J.-S.,
McBlroy,K.E., Choi,P.S., Harada,J.J., Fischer,R.L. and
Goldberg,R.B.
                                                                                                                                                   Score 21; DB 14; Length 309;
Pred. No. 2.8e+03;
0; Mismatches 5; Indels
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Seq primer: 5' TriplEx
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l Similarity 82.8%;
24; Conservative
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Matches 24; Conserva
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CA907970
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70.0%; Score 21; DB 14; Length 430;

Query Match

O; Gaps Best Local Similarity 82.8%; Pred. No. 2.6e+03; Matches 24; Conservative 0; Mismatches 5; Indels

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Search completed: May 26, 2004, 22:26:53 Job time : 2084.59 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

May 26, 2004, 15:22:28 ; Search time 199.949 Seconds (without alignments) 594.900 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-676-299-4' 28 1 caacacataaccaaaaacgcatatgatt 28

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1980s; genesequ1990s; genesequ2001as; genesequ2001bs; genesequ2001bs; genesequ2003as; genesequ2003as; genesequ2003as; genesequ2003as; genesequ2003s; 29Jan04:\* N. Geneseq 2

1. genesequ 3

2. genesequ 4: genesequ 6: genesequ 7: genesequ 7: genesequ 7: genesequ 9: genesequ 10: genes Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Acd28585 E. coli A	Acd28584 E. coli A	Acd28589 E. coli A	Acd28588 E. coli A	Abk28137 DNA trans	Aaa81455 N. mening	Continuation (15 o	Continuation (14 o	Aaf21610 Neisseria	Aaf56298 IS2 eleme	Aaz67933 Human map	Aag67726 Comamonas	Abl87877 Human ova	Abl32742 Human imm	Aah52751 S. epider	Aaf91383 N. mening	Abk37763 DNA seque	Aba02964 Human rib	Ada32102 DNA encod	Aah54693 S. epider	Aah54720 S. epider	Aav10663 Mouse Fas	Aac87652 Mouse liv
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% Query Match	100.0	100.0	75.0	75.0	73.6	73.6	73.6	73.6	73.6	71.4	70.0	70.0	68.6	68.6	67.9	67.9	6.7.9	67.9	67.9	67.9	67.9	67.9	67.9
Score	28	28	21	21	20.6	20.6	20.6	20.6	20.6	20	19.6	19.6	19.2	19.2	19	19	19	19	<b>1</b>	6 <b>F</b>	19	19	19
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AAL49583 AB(7)5766 AAS33419 AAL05045 ABL97938	ABK40025 AAS46774 ADA13411_2 AAT42063_12	ADA29013 ABQ69002 ABQ14038 ABQ14039 ABQ13769	ABQ13768 ACF68832 ABD10524 ABL16815 AAC69498	ABZ15671 ADB68950 ABL08236
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9058 9058 12103 12103	17534 34769 110000	459 678 816 816 817	817 1068 1102 1137 1338	1947 3227 7803
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67.9	67.9	666.4 4.666.4 4.4.4.4	4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4	66.4 66.4 66.4
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		18.6 18.6 18.6 18.6	188.6 188.6 18.6 18.6	18.6 18.6 18.6
4 5 5 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6	00100	30000	8 8 4 4 4	4 4 4 5 4 5
0 0	טט	000	00000	U
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## ALI GINMENTS

RESULT 1

BP. ACD28585 standard; DNA; 28

ACD28585;

(first entry) 10-OCT-2003 E. coli ArsR binding oligonucleotide PLASLIB.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003.

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

(LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the areance resistance operon of E. coli) protein comprising an amino acid sequence that is at least 90% identical to anno acids 1-97 of the ArsR sequence appearing as ABUG3440 binding to a nucleic acid ACD 85.85

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Gaps

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Indels

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Mismatches 28

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Conservative

28;

Matches

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1 CAACACATAACCAAAAACGCATATGATT

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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein content in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and an Arsk (encoded by part of the arsenic resistance operon of B. coli) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as Aug 340 binding to a nucleic acid sequence appearing as Aug 340 binding to a nucleic acid sequence comprising oligonuclectides appearing as ACD 38584-ACD 38591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligonuclectide which binds to a plantid expressed Arsk protein and is used in the biosensor of the
                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.
sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds to a plasmid expressed Arsk protein and is used in the biosensor of the
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                         ö
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArsR; arsenic resistance operon; biosensor; ss; arsenic.
                                                                                                                                                             8; Length
                                                                                                                  Sequence 28 BP; 14 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                           Query Match
100.0%; Score 28; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B. coli ArsR binding oligonucleotide PLASLIT.
                                                                                                                                                                                                                                                                   1 CAACACATAACCAAAAACGCATATGATT 28
                                                                                                                                                                                                                                             1 CAACACATAACCAAAAACGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 35; Page 15; 36pp; English.
                                                                                                                                                                                                                                                                                                                                           RESULT 2
ACD28584/c
ID ACD28584 standard; DNA; 30 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-2002; 2002US-00222952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-2001; 2001US-0313714P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-576876/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LAIN/) LAING L G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003096275-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                               ACD28584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laing LG;
  88888888
                                                                                                                                                                                                                                                                                  g
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Score 28; DB 8; Length 30; Pred. No. 0.07;

100.0%;

Query Match Best Local Similarity

Sequence 30 BP; 5 A; 2 C; 7 G; 16 T; 0 U; 0 Other;

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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specifically binds the analyte; (2) an isolated nucleic acid containing a containing a specific binding sequence that is bound specifically by the protein; and contained are a biosensor device for detecting the presence of the analyte. Also included are a consort of the arsenic resistance operon of E. coli) protein comprising an acid sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as ABG3440 binding to a nucleic acid comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds to a plasmid expressed Arsk protein and is used in the biosensor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

75.0%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         ArsR; arsenic resistance operon; biosensor; ss; arsenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 10 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                     E. coli Arsk binding oligonucleotide PLASSIB
CAACACATAACCAAAAACGCATATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 TAACCAAAACGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TAACCAAAACGCATATGATT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 35; Page 15; 36pp; English.
                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   뮵.
                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001; 2001US-0313714P.
                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-2002; 2002US-00222952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
ACD28588/c
ID ACD28588 standard; DNA; 23
                                                                                                         ACD28589 standard, DNA; 21
                                                                                                                                                                                 10-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-576876/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid in the presence
analyte in a sample.
                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                   US2003096275-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LAIN/) LAING L
                                                                                                                                                                                                                                                                                                                                                                         22-MAY-2003
                                                                                                                                               ACD28589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laing LG;
                                                                     ACD28589
                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
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system comprising isolated protein and nucleic acid, and a detection tem that indicates a change in binding of the protein to the nucleic d in the presence of the analyte, useful for detecting the presence of
                                                    ArsR; arsenic resistance operon; biosensor; ss; arsenic.
                                     E. coli ArsR binding oligonucleotide PLASSIT
                                                                                                                  15-AUG-2002; 2002US-00222952.
                                                                                                                                  20-AUG-2001; 2001US-0313714P
                     10-OCT-2003 (first entry)
                                                                                                                                                                               WPI; 2003-576876/54.
                                                                                                                                                                                                                       analyte in a sample.
                                                                                                                                                 (LAIN/) LAING L G.
                                                                   Escherichia coli.
                                                                                   US2003096275-A1
                                                                                                   22-MAY-2003
                                                                                                                                                                Laing LG;
        ACD28588
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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the mucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and are a carried to the arsenic resistance operon of B. coli) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid sequence appearing as ABU63440 binding to a nucleic acid system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligonuclectide which binds to a plasmid expressed ArsR protein and is used in the biosensor of the Sequence 23 BP; 5 A; 2 C; 4 G; 12 T; 0 U; 0 Other; Claim 35; Page 15; 36pp; English. invention

Gaps ö Score 21; DB 8; Length 23; Pred. No. 43; 0; Indels 100.0%; Pred. w. 75.0%; 21; Conservative Similarity Query Match Local Matches

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28 23 TAACCAAAAACGCATATGATT TAACCAAAAACGCATATGATT Φ

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ABK28137 standard; DNA; 6391 ABK28137; 

(first entry) 23-APR-2002 DNA transcription associated genomic DNA #6.

DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA, cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer;

immunological disorder; Werner syndrome; developmental disorder; psoriasis, Rieger's syndrome; neurological disorder; erythropolesis; neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; anglogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour. infection; Sezary syndrome; haematological disorder; tuberculosis;

Unidentified.

WO200192565-A2.

06-DEC-2001.

06-APR-2001; 2001WO-EP003973

06-APR-2000; 2000DE-01019058.

07-APR-2000; 2000DB-01019173. 30-JUN-2000; 2000DB-01032559. 01-SEP-2000; 2000DB-01043826.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2002-090046/12.

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Wenner syndrome, psoriasis, myocardial infarction, solid tumors or

Claim 1; SEQ ID NO 11; 32pp; English

The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer that hybridises to or is identical or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, the methylation status) and sorders, merner syndrome, the methylation associates, syndrome, mycocardial disorders, neurological disorders, provinasis, Rieger's syndrome, cuberculosis, developmental disorders, psychatome, mycocardial infarction, hypertension, angiogenesis, congenital heart disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours associated genomic DNA molecules of the printed specification but associated genomic DNA molecules of the printed specification but associated in electronic format directly from the European Patent 

Sequence 6391 BP; 1421 A; 156 C; 1688 G; 3126 T; 0 U; 0 Other;

Gaps ö DB 6; Length 6391; 4; Indels 73.6%; Score 20.6; I 85.2%; Pred. No. 89; iive 0; Mismatches Conservative Local Similarity tes 23; Conserv Query Match Matches

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RESULT 6

AAA81455 standard, DNA; 23532 AAA81455 ID AAA8 XX AC AAA8

AAA81455,

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Isolated nucleotide seguences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea.
                                                                                                                                                                                               Tettelin H, Venter JC;
Ratti G, Scarselli M, Scarlato V;
                                          Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
                        meningitidis partial DNA sequence gnm_3 SEQ ID NO:3.
                                                                                                                                                                                                                                                                                      Claim 7; Page 253-260; 1760pp; English.
                                                                                                                                                                                               Hickey B, Peterson J,
Galeotti C, Mora M,
                                                                                                                                                  9BUS-0103794P
                                                                                                                                  99WO-US023573
                                                                                                                                                            99US-0132068P
       04-DEC-2000 (first entry)
                                                                              Neisseria meningitidis.
                                                                                                                                                                                                      Masignani V, Galeott
Rappuoli R, Pizza M;
                                                                                                                                                                            (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                  WPI; 2000-318079/27.
                                                                                              WO200022430-A2
                                                                                                                                 08-OCT-1999;
                                                                                                                                                  09-OCT-1998;
30-APR-1999;
                                                                                                               20-APR-2000,
                                                                                                                                                                                                 Frazer CM,
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA81244 represent specifically claimed Neisseria meningitidis genomic DAA sequences. AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DAAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DAAA81304 to AAA81303 and AAB25620 to AAA81254 to AAA81259 and AAA81304 to AAA81301 represent PCR primers used in the isolation of Neisseria meningitidis DAN sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis DAN sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis DAN sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis DAN sequences; and AAA81322 to AAA81452 represent CC Neisseria protein sequences, and antibodiss against them, can be used in the exemplification of the present invention. The uncleic acid sequences, protein sequences, and antibodiss against them, can be used in the manufacture of a medicament) for treating, concent (or in the manufacture of amedicament) for treating, or preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identification of sequences from the bacterium of pathogenic Neisseriae. Identification of sequences from the bacterium villaso facilitate production of biological probes, particularly or accines have failed mainly due to antigen tolerance. Multivalent corries have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not that may be presumed targets for the immune system and which are antigenically variable or at least more conserved than other more

Sequence 23532 BP; 6919 A; 5186 C; 5000 G; 6427 T; 0 U; 0 Other;

Gaps ő DB 3; Length 23532; 4; Indels 73.6%; Score 20.6; I 85.2%; Pred. No. 96; iive 0; Mismatches 23; Conservative Local Similarity Query Match Matches

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RESULT 7 AAA81490\_14

AAA61490 13
Continuation (14 of 15) of AAA81490 from base 1300001 (N. meningitidis B full length
Continuation (14 of 15) of AAA81490 from base 1300001 (N. meningitidis B full length
WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490
WP AAA81490\_00 110000 from base 1400001 (N. meningitidis B full length LOCUS AAA81490 Accession Aaa81490 ö Ö Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial; Gaps Gaps Score 20.6; DB 3; Length 110000; Pred. No. 1.1e+02; 0; Mismatches 4; Indels 0; ö DB 3; Length 37668; Neisseria meningitidis B nucleotide sequence SEQ ID NO:111. Indels Score 20.6; Di Pred. No. 99; 0; Mismatches 109361 AACAATAACCATAATGCATATCATT 109387 9361 AACAAATAACCATAAATGCATATCATT 9387 2 AACACATAACCAAAAACGCATATGATT 28 2 AACACATAACCAAAAACGCATATGATT 28 210000 310000 410000 610000 910000 1110000 1210000 1310000 110000 210000 310000 510000 610000 710000 131**0**000 141**0**000 110000 510000 1437668 810000 910000 110000 1210000 AAF21610 standard, DNA; 349980 BP. of 15) of AAA81490 into 15 fragments Match 73.6%; Local Similarity 85.2%; Les 23; Conservative ch 1 Similarity 85.2%; 23; Conservative 100001 200001 300001 400001 500001 700001 800001 900001 1000001 1100001 1200001 1300001 200001 300001 400001 500001 600001 1100001 1200001 1300001 700001 100001 900001 800001 000000 Begin Neisseria meningitidis. Continuation (15 of 15)
WP Sequence split into 1
WP Fragment Name
WP AAA81490\_00 Local Similarity AAA81490 00 AAA81490 01 AAA81490 02 AAA81490 03 AAA81490 04 AAA81490 05 AAA81490 10 AAA81490 11 AAA81490 12 AAA81490 13 AAA81490 13 AAA81490 00
AAA81490 01
AAA81490 03
AAA81490 03
AAA81490 04
AAA81490 05
AAA81490 05
AAA81490 05 AAA81490 07 AAA81490 08 AAA81490 09 AAA81490\_12 AAA81490\_13 AAA81490\_14 AAA81490\_09 AAA81490\_10 AAA81490\_1 13-MAR-2001 AAF21610; Query Match Query Match Best Loc Matches Best Loc Matches RESULT 9 RESULT g 8 g ઠ

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The present invention describes the full length genome of Neiseeria

meningitidis B (NMB). The sequences in AAP21544 and AAP21607 to AAP21613

crepresent fragments of the NMB genomic sequence, as the sequence was too

long to go in a record on its own it was split into 8 sequences which

coverlap each other at the beginning and end of each sequence by 49980 bp

(i.e. the last 49980 bp of AAP21544 is repeated at the beginning of

AAP21607, the last 49980 bp of AAP21549 are repeated at the beginning of

AAP21607, the last 49980 bp of AAP21589 encode the Neisseria proteins

given in AABS8550 to AABS8593, and AAP21589 to AAP2160 represent FOR

CC primers which are used in the exemplification of the present invention.

The NMB genome and fragments from it have antibacterial activity, and can

compute antibodies which binds to the proteins can be used in compositions

conditions arised to Neisserial bacteria or as a

diagnostic reagent for detecting the presence of Neisserial bacteria or

of antibodies raised to Neisserial bacteria or as a

conduter storage medium or computer databases can be used in a search to

identify open reading frames (ORFS) or coding sequences within the NMB

genome. The DNA sequences provide further opportunities to find antigenic
                                                                                                                                                                                                                                                                                                    Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis B full length genome sequence and open read:
frames are used to detect, treat and prevent Neisserial infections
                                                                                                                                                                                                                                                                               Venter JC;
Scarselli M,
                                                                                                                                                                                                                                                                               Tettelin H,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outer membrane proteins currently used
                                                                                                                                                                                                                                                                               Peterson J, Tetti C, Mora M, CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Appendix A; 692pp; English
                                                                                                                                      30-APR-1999; 99US-0132068P.
08-OCT-1999; 99WO-US023573.
28-FEB-2000; 2000GB-00004695.
                                                                                                08-MAR-2000; 2000WO-US005928
                                                                                                                                                                                                                   (CHIR ) CHIRON CORP.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                               Pizza M, Hickey E, Pet
Masignani V, Galeotti C
Rappuoli R, Frazer CM,
                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-647603/62
                   WO200066791-A1.
                                                           09-NOV-2000
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ö Seguence 349980 BP; 86771 A; 92803 C; 86340 G; 84066 T; 0 U; 0 Other; Gaps Score 20.6; DB 3; Length 349980; Pred. No. 1.1e+02; 0; Mismatches 4; Indels 0; 73.68; 85.28; Best Local Similarity 85.2 Matches 23, Conservative Query Match

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Miniature inverted repeat transposable element; MITE; duplication; regulate; IS2; ds.

The present invention relates to a miniature inverted-repeat transposable element (MITE)-like element capable of causing duplication of a target sequence at the site of its insertion in a genomic gene. The invention is useful for causing expression of a transgene in a plant. It can also be used for inducing or regulating the expression in a plant of the gene Novel miniature inverted-repeat transposable element (MITE)-like element useful for constructing transgene expression cassette for stably creating genetically engineered organisms capable of expression of transgene. Gaps ö Length 1543; Seguence 1543 BP; 569 A; 244 C; 214 G; 516 T; 0 U; 0 Other; 5; Indels 71.4%; Score 20; DB 4; I Similarity 82.1%; Pred. No. 1.4e+02; 23; Conservative 0; Mismatches 5; Disclosure, Page 103-104; 104pp; English Koda T; Fukuda T, 19-JUL-2000; 2000WO-JP004837. 21-JUL-1999; 99JP-00206316. 21-JUN-1999; 99JP-00206320. 12-JUN-2000; 2000JP-00175825. (SANE-) SAN-BI GEN FFI INC. (OZEK/) OZEKI Y. Ozeki Y, Oyanagi M, WPI; 2001-147351/15. WO200105986-A2 23; introduced Query Match Local Matches 

360 CCACACATAATCAAAATCACATATAATT 333 BP AAZ67933 standard; DNA; 47 AAZ67933; RESULT 11 AAZ67933, g

(first entry)

10-SEP-2001

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CAACACATAACCAAAAACGCATATGATT

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Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds. /standard\_name= "single nuclectide polymorphism" Human map-related biallelic marker SEQ ID NO:2280. Location/Qualifiers replace (24, A) Homo sapiens variation 

99WO-IB000822 RO9954500-A2 1-APR-1999; 28-OCT-1999

98US-0082614P 21-APR-1998; 23-NOV-1998;

(GEST ) GENSET

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AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ740 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3050, as not a contain on a sequence in the Sequence Listing from the
                                                                    Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scubrier F;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 19.6; DB 3; Length 47; Pred. No. 1.6e+02; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nylon 6.6;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47 BP; 13 A; 3 C; 8 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amidase; ammonium adipamate; diammonium adipate;
5-cyanovaleramide; 5-cyanovalerate; caprolactam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cerbelaud E, Le Coq A, Levyschil S, Petre D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comamonas testosteroni NI 1 amidase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ACACATAACCAAAAACGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 AAACATAAACAAAATGCATATAATT 22
               Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127. ,1383
/*tag= a
/product= "amidase"
                                                                                                                Claim 3; Page 717; 2745pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ67726 standard; DNA; 1491 BP.
                                                                                                                                                                                                                                                                                                                                                                                                         70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comamonas testosteroni; NI 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-FR000080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POULENC CHIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Conservative
              Blumenfeld M,
                                                                                      map of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [revised]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-264103/32.
P-PSDB; AAR60155.
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                          WPI; 2000-013267/01.
                                                                                                                                                                                                                                                                                                                                                      present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RHON ) RHONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WC9417190-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ67726;
               Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
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Gaps

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                                                                                                                                                                                                                                                         library using a degenerate probe based on the N-terminal amino acid sequence of the purified enzyme. The amidase is able to hydrolyse amides to carboxylates and has higher activity on ammonium adipamate than on adipamate than on adipamate to diammonium adipate for production of nylon 6,6 or for converting 5-cyanovaleramide to 5-cyanovaleramide to 5-cyanovaleramide to 5-cyanovaleramide to 5-cyanovaleramide to 5-cyanovaleramide to 5-cyanovaleramide (an intermediate for caprolated and intermediate for field.) (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                          The amidase gene was isolated from a Comamonas testosteroni genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                          New amidase with greater activity on adipamate than on adipamide - a related DNA and microorganisms producing it, partic used to produce ammonium adipate or 5-cyanovalerate for nylon mfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or I cell expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.6; DB 2; Length 1491; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 1491 BP; 546 A; 239 C; 262 G; 444 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian cancer related cDNA clone SEQ ID NO:10855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%; bcc.
84.6%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 10855; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1025 AAAATATAACCAAAGACGAATATGAT 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones R;
                                                                                                                                                                      Claim 3; Fig 2; 55pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7877/c
ABL87877 standard; cDNA; 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-2001; 2001WO-US017756.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Algate PA, Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.6
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-122075/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200192581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL87877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL677/C

ABL67/A

AC ABL67

AC ABL6
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8
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Gaps

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Length 8087;

Score 19.2; DB 6; Length 8
Pred. No. 3.3e+02;
0; Mismatches 3; Indels

(first entry)

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WO200200928-A2.
                                                                    Homo sapiens.
                                                                          03-JAN-2002.
                                                                                                   methylation.
                                           ABL32742;
                      Query Match
                                     RESULT 14
ABL32742/c
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Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                    S. epidermidis open reading frame nucleotide sequence SEQ ID NO:895
                             Sequence 8087 BP; 2081 A; 179 C; 1817 G; 4010 T; 0 U; 0 Other;
                                                                                                                                                                                     675 CAACACTTAAATAAAAACGCATAT 652
                                                                                                                                                1 CAACACATAACCAAAAACGCATAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-2000; 2000WO-US030782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1999; 99US-0164258P.
                                                                Query Match
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                     AAH52751 standard; 'DNA; 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                              03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2001
                                                                                                                                                                                                                                                                                                                           AAH52751;
                                                                                                                                                                                                                                                RESULT 15
AAH52751/c
            ×8
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                                                                                                                                                                                     쉱
                                                                                                                                                                                                                                                                                       sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tunnour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of ribozyme molecules for inhibiting to isolate a full length gene from a suitable library e.g., a tumour cells; and library using well known techniques
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alz, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                       Length 343;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                Sequence 343 BP; 117 A; 52 C; 50 G; 124 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 715; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 715.
                                                                                                                                                                                                                                                                                   Match 68.6%; Score 19.2; DB 6; 1 Local Similarity 87.5%; Pred. No. 2.7e+02; es 21; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                  5 ACATAACCAAAACGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                        103 ACATAACTAAAAGGCATCTGATT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL32742 standard; DNA; 8087 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-130909/17
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AASIS2304 to AAR53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and lin can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. containing the used to produce hosts cells which express the which are used to produce hosts cells which express the college of the polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. Comparation of the polypeptides and sisone used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis AAK53971 to treatment of S. epidermidis infections, e.g. endocarditis path53971 to CC AAH55090 represent specifically claimed S. epidermidis genomic DNA CC polymucleotide sequences from the present invention. AAH55091 to AAH55098 corpresent specifically claime all the polymucleotide sequences and primers which are used in the specifically claims all the polymucleotide sequences given in the specifically claims all the polymucleotide sequences given in the specifically only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                          Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
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Pred. No. 3.4e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 945 BP; 390 A; 102 C; 184 G; 269 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                  Claim 8; Page 267; 2188pp; English.
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nilarity 81.5%;
Conservative 0
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Best Local Similarity
Matches 22; Conserva
WPI; 2001-316495/33.
                                          P-PSDB; AAG81901.
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Thu May 27 10:11:40 2004

Search completed: May 26, 2004, 17:50:01 Job time: 201.949 secs

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- nucleic search, using sw model OM nucleic

May 26, 2004, 16:18:00 ; Search time 44.6325 Seconds (without alignments) 348.146 Million cell updates/sec Run on:

US-10-676-299-4

1 caacacataaccaaaacgcatatgatt 28 Title: Perfect score: Sequence:

Scoring table: IDENTITY NUC Gapox 10.0

Total number of hits satisfying chosen parameters:

632709 segs, 277475446 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued\_Patents NA:\*
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIBS

Description	Sequence 2280, Ap	33		ri o	e i	e 1,		1957	m	19	κ K	7	12,	2	5, A	23	1464,	16,	178	7	'n	'n	-ì	e,	e,	ų,	m
ΙΩ	US-09-422-978-2280	US-09-328-352-3389	US-08-913-014A-9	US-09-653-285-9	US-09-557-884-1	US-09-643-990A-1	US-09-328-352-300	US-09-107-532A-1957	US-10-204-708-39	US-09-134-001C-1995	US-09-734-674-3	US-09-227-357-119	US-08-139-937-12	PCT-US93-11310-12	US-08-328-254-5	US-09-976-594-538	US-09-107-532A-1464	US-09-349-740A-16	US-09-539-333D-178	US-09-349-740A-1	US-09-873-404-3	US-09-984-890-3	US-09-790-988-1	US-09-751-389-3	US-09-718-841-3	US-09-718-810-3	US-09-718-854-3
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* Query Match Length	47	2481	9058	9058	1830121	1830121	459	567	19513	1026	202001	1442	4868	4868	8789	1253	2061	2911	3001	4500	63588	75395	640681	786431	1070	1070	1070
* Query Match	68.6	67.9	67.9	67.9	67.3	67.1	66.4	65.7	64.3	63.6	63.6	62.9	62.9	62.9	62.9	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	61.4	61.4	61.4
Score	19.2	19	19	19	18.8	18.8	•	18.4	18	17.8	17.8	17.6	17.6	17.6	17.6	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.2	17.2	17.2
ult No.	H	7	m	4	ហ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	13	50	23	22	23	24	25	56	23
Result No.	¦ 0	บ	υ	υ			υ	υ	υ		O	υ	O	O	υ				U						υ	υ	U

C 28 17.2 61.4 1689 4 US-09-718-841-1 C 29 17.2 61.4 1689 4 US-09-718-8410-1 C 31 17.2 61.4 1689 4 US-09-718-810-1 C 31 17.2 61.4 2418 4 US-09-620-312D-158 C 32 17.2 61.4 5418 4 US-09-620-312D-158 3 17.2 61.4 564976 4 US-09-620-312D-158 3 17.2 61.4 1664976 4 US-09-716-421B-1 3 17.2 61.4 1664976 4 US-09-716-421B-1 3 17.6 0.7 653 4 US-09-716-421B-1 3 17.6 0.7 653 4 US-09-671-124B-313 3 17.6 0.7 653 4 US-09-671-124B-313 3 17.6 0.7 653 4 US-09-639-184-313 3 17.6 0.7 653 4 US-09-312-283C-260 40 17.6 0.7 2800 3 US-09-312-283C-260 41 16.8 60.0 271 4 US-09-313-294A-6454 C 44 16.8 60.0 774 3 US-09-313-294A-6454 C 45 16.8 60.0 774 3 US-08-221-767-1	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 158, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 313, App	Sequence 313, App	Sequence 313, App	Sequence 313, App	Sequence 313, App		Sequence 260, App	Sequence 13, Appl	Sequence 1, Appli	Sequence 6454, Ap	Sequence 5, Appli	Sequence 1, Appli	
28 17.2 61.4 4.1 61.2 61.4 4.1 60.7 4.2 61.4 60.0 61.4 61.4 61.4 61.4 61.4 61.4 61.4 61.4	US-09-718-841-1	US-09-718-810-1	US-09-718-854-1	US-09-620-312D-158	US-08-545-528D-1	US-08-916-421B-1	US-09-702-705-313	US-09-736-457-313	US-09-614-124B-313	US-09-671-325-313	US-09-589-184-313	US-09-188-930-260	US-09-312-283C-260	US-08-487-826B-13	US-08-545-528D-1	US-09-313-294A-6454	US-09-325-932A-5	US-08-221-767-1	
28 17.2 61.4 4.1 61.2 61.4 4.1 60.7 4.2 61.4 60.0 61.4 61.4 61.4 61.4 61.4 61.4 61.4 61.4	4	4	4	4	47	4	4	4	4	4	4	m	4	N	4	4	7	m	
28 17.2 29 17.2 31 17.2 32 17.2 33 17.2 34 17.2 34 17.2 34 17.2 34 17.2 34 41 17.2 41 17.2 41 16.8 44 16.8 45 16.8	1689	1689	1689	2418	580073	1664976	653	653	653	653	653	2800	2800	19124	580073	271	483	774	
28 17.2 29 17.2 31 17.2 32 17.2 33 17.2 34 17.2 34 17.2 34 17.2 34 17.2 34 41 17.2 41 17.2 41 16.8 44 16.8 45 16.8	4,	4	4.	4.	4.	4	۲.	۲.		۲.		7	7	۲.		0	0	0	
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0000 0000 0000000000000000000000000000	17.2	17.2	17.2	17.2	17.2	17.2	17	17	17	17	17	17	17	17	17	16.8	16.8	16.8	
0000	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
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## ALIGNMENTS

18-19-42.2.978-2.2801/C 18-19-42.2.978-2.2801/C 18-19-10-10-10-10-10-10-10-10-10-10-10-10-10-	09-422-978-2280/c Sequence 2280, Application US/09422978 Batent No. 6537751 GENERAL INFORMATION: APPLICANT: Cohen, Daniel APPLICANT: Chumakov, Ilya TITLE OF INVENTION: Biallelic markers for use in constructing FILE REFERENCE: GENSET.020Cp1 CURRENT APPLICATION NUMBER: US/09/422,978 CURRENT PILING DATE: 1999-10-20 EARLIRE APPLICATION NUMBER: US/09/298,850 PARITES APPLICATION NUMBER: 1994-40-21	onstructing	a hiç	high density
EARLIER FILING DATE: 19 EARLIER APPLICATION NUM EARLIER PILING DATE: 19 NUMBER OF SEQ ID NOS: 1 NUMBER OF SEQ ID NOS: 1 TYPE: DNA TYPE: DNA ORGANISM: HOMO Sapiens FRATTRE: NAME/KEY: allele LOCATION: 24	EARLIER FILING DATE: 1996-11-23 EARLIER PILING DATE: 1996-11-23 EARLIER PILING DATE: 1998-04-21 NUMBER OF SEQ ID NOS: 11796 EQ ID NO 2280 ILENGTH: 47 TYPE: DNA ORGANISM: Homo Sapiens FEATURE: NAME/KEY: allele NAME/KEY: allele OCCATION: 24	ಭ ಬ ೦ ೯೪		
, Olffer interestrict. US-09-422-978-2280 Query Match Best Local Similarity Matches 21, Conser	68.6%; Score 19.2; DB 4; Brity 80.8%; Pred. No. 15; Onservative 1; Mismatches 4;			Gaps 0;
Oy 3 ACI   	3 ACACATAACCAAAAAGGCATATGATT 28 			

RESULT 2
US-09-128-352-3189/c
| Sequence 3389, Application US/09328352
| Sequence 3389, Application US/09328352
| Patent No. 6562958
| GENERAL INFORMATION:
| APPLICANT: GENTY L. Breton et al.
| TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: GFC99-039A
| CURRENT APPLICATION NUMBER: US/09/328,352
| CURRENT PILING DATE: 1999-06-04
| NUMBER OF SEQ ID NOS: 8252

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Query Match 67.9%; Score 19; DB 4; Length 9058; Best Local Similarity 81.5%; Pred. No. 37; Matches 22; Conservative 0; Mismatches 5; Indels
                      Sequence 9, Application US/09653285
Patent No. 6590090
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hishi, Kazunori
Shintani, Yasushi
TITLE OF INVENTION:
PRODUCTION AND USE
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David G. Conlin, Esq.
DIKE, BRONSTEIN, ROBERTS & USHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: PASSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/653,285
FILING DATE: 31-Aug-2000
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/913,014
FILING DATE: «URKNOWN)
ATTORNEY/AGENT INFORMATION:
RAME: DATIG CONINI NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 342/47694
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8604 AACAATAAACAAAGCACAAATGATT 8578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPLOGY: LINEAR NOLECULE TYPE: Genomic DNA SEQUENCE DESCRIPTION: SEQ 1D NO: 9: US-09-653-285-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TBLEX: <UNKNOWD>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 25
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Sequence 9, Application US/08913014A

Sequence No. 6235878

GENERAL INFORMATION:
APPLICANT: Nishi, Kazunori
APPLICANT: Bixichi, Yukiko
ITILE OF INVENTION: PRODUCTION AND USE
ITILE OF INVENTION: PRODUCTION AND USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: David G. Conlin, Esq.
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & USHMAN, LLP
STREET: 130 Water Street

CITY: Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.9%; Score 19; DB 3; Length 9058; Best Local Similarity 81.5%; Pred. No. 37; Matches 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                             Query Match 67.9%; Score 19; DB 4; Length 2481;
Best Local Similarity 81.5%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER SIDENCE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,014A
PILING DATE: 04-SEP-1997
CLASSIFICATION NATA:
APPLICATION NUMBER: PCT/JP97/02480
PILING APPLICATION NUMBER: PCT/JP97/02480
PILING APPLICATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 342/47694
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESTAX: 617-523-5440
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LEMETH: 9058
TWENTH: 9058
                                                                                                                                                                                                                                                                        2 AACACATAACCAAAACGCATATGATT 28
; SEQ 1D NO 3389
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-913-014A-9
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CITY: Boston, STATE: MA COUNTRY: USA

IS-09-653-285-9/c

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APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influencae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
                     Sequence 1, Application US/09557884; Patent No. 6506581; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
US-09-557-884-1
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Gaps

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8604 AACAAATAAACAAAAGCACAAATGATT 8578

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RESULT 4

2 AACACATAACCAAAAACGCATATGATT 28

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2 AACACATAACCAAAAACGCATATGATT 28

TYPE: Nucleic acid STRANDEDNESS: Double

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J. Craig Venter
J. Craig Venter
IITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
STREET: 9410 Key West Avenue
STATE: MD
COUNTRY: USA
ZATE: DAID Pentium
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/09/643,990A
FILING DAIE: 23-Aug-2000
CLIASSIFFCATION: CURRIOWN>
PRIOR APPLICATION NUMBER: 08/487,429
FRING APPLICATION NUMBER: 08/487,429
FRING DAIE: 1995-06-07
APPLICATION NUMBER: 08/487,429
FILING DAIE: 1995-06-07
FILING DAIE: 1995-06-07
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Deal Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION NUMBER: 08/476,102
RILING DATE: 15-Apr-2000
PRIOR APPLICATION NUMBER: 08/476,102
FILING DATE: 1509-5
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: P1995
ATTORNEY/AGENT INFORMATION:
TELEPHANE: 301-309-8504
TELEPHANE: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TWPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.1%; Score 18.8; D
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-557-884-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1238890 ATAACCAAAAACGCATATTGTT 1238911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ATAACCAAAACGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/03643990A; Patent No. 6528289; GENERAL INFORMATION:
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US-09-643-990A-1
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TB-T0-0/0-07-81

TUM WEY 2/ IN: LI:40 2004

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Sequence 300, Application US/09328352

Patent. No. 6562958
GRANEAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GT-99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 300
ILENGTH: 459
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US-09-107-532A-1957/c
; Sequence 1957, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: TITLE OF INVENTION:
-- 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.4%; Score 18.5; D
Best Local Similarity 84.0%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ 1D NO: 1: US-09-643-990A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1238890 ATAACCAAAAACGCATATTGTT 1238911
INDORMATION TO SECURE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CACATAACCAAAAAGGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 CACATAACAAAAACGCAACTGAAT 74
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOPTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ATAACCAAAAACGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Acinetobacter baumannii US-09-328-352-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-328-352-300/c
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Gaps

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Score 18; DB 4; Length 19513; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rred. No. 88;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.6%; Score 17.8; Best Local Similarity 90.5%; Pred. No. 88; Matches 19; Conservative 0; Mismatches
                                                                                                                                                  18377 AAAACATAATCAAAACCGAATATAAT 18352
                                                                                                       2 AACACATAACCAAAAACGCATATGAT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175136 CATAACCAAAAAAGCATAGGA 175116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rype: DNA Caphylococcus epidermidis US-09-134-001C-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602 TAACTAAAAAAGCATATGATT 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 TAACCAAAAACGCATATGATT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 CATAACCAAAACGCATATGA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc_feature

) LOCATION: (1) ... (202001)

) OTHER INFORMATION: n = A,T,C or G

US-09-734-674-3
         Query Match
Best Local Similarity 80.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.5'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                  RESULT 10
US-09-134-001C-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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Patent No. 6677731

GENERAL INFORMATION:

APPLICANT: PIEPENROCK, Christian

TITLE OF INVENTION: Dy Assessing DNA Methylation

FILE REPRENCES: 6013-101.2

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT APPLICATION NUMBER: US/10/3071

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

LENGTH: 19513

"WHERE OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.7%; Score 18.4; DB 4; 78.6%; Pred. No. 45; trive 0; Mismatches 6;
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1996

PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05151
FILING DATE: 319 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATIAIGLIO, PEMBLA DEDEKE
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1957:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 Dase pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc_feature

; LOCATION: (B) LOCATION 1...567

; SEQUENCE DESCRIPTION: SEQ ID NO: 1957:

US-09-107-532A-1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAACACATAACCAAAACGCATATGATT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.69
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
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US-10-204-708-39/c
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Sequence 1995, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICATY: Lyan Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU:

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR PILING DATE: 1997-11-08

PRIOR PILING DATE: 1997-08-14

PRIOR PILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-734-67-3/c
INC-09-734-67-3/c
Sequence 3, Application US/09734674
Sequence 3, Application US/09734674
Sequence 3, Application US/09734674
GARREAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFRENCE: CLO01018
CURRENT APPLICATION NUMBER: US/09/734,674
SUGNERAL PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PRECED FOR Windows Version 4.0
SEQ ID NO 3
LENGTH: 202001
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us-10-676-299-4.rni

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Sequence 119, Application US/09227357

Sequence 119, Application US/09227357

Petern No. 6342891

GENERAL INCORMATION 123 Human Secreted Proteins TITLE OF INVENTION; 129 Human Secreted Proteins Human Secreted Proteins Title Of Invention; 129 Human Secreted Proteins Earlier Fitting Office 129 Human Secreted Proteins Earlier Fitting Office 129 Human Secreted Protein
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Gaps ö 62.9%; Score 17.6; DB 4; Length 1442; ilarity 83.3%; Pred. No. 1.1e+02; Conservative 0; Mismatches 4; Indels 0; US-08-13-9-937-12/c

| Sequence 12, Application US/08139937
| Sequence 12, Application US/08139937
| Patent No. 5821070
| GENERAL INFORMATION:
| APPLICANT: LEE, WEN-HWA | APPLICANT: SHAW BEI | TITLE OF INVENTION: RETINOBLASTOWA-ASSOCIATED PROTEINS | TITLE OF INVENTION: RETINOBLASTOWA-ASSOCIATED PROTEINS | NUMBER OF SEQUENCES: 14 | CORRESPONDENCE ADDRESS: ADDRESSERE: CAMPBELL AND FLORES COMPUTER TRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
COMPUTER: Plan PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/139,937
FILING DATE: 20-OCT-1993
CLIASSIFICATION NUMBER: US 07/979,156
FILING DATE: 20-OCY-1992
ATTORNEY/AGRNT INPORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 9-CJ 9370
TELEFORMICATION NUMBER: 9-CJ 9370
TELEFORMICATION INFORMATION:
TELEFORMICATION NUMBER: 13-55-9001
TELEFORMICATION NUMBER: 1619-535-9001
TELEFORMICATION POR SEQ 1D NO: 12:
SEQUINCE CHARACTERISTICS: ALUKESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
STATE: CALLIFORNIA
COUNTRY: USA
COMPIEN: CALLIFORNIA
ZIP: 92122 774 ACACCATAAACAATATGATT 751 EARLIER APPLICATION NUMBER: 60,058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID MOS: 672
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 119
LENGTH: 1442 TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KYS SITE
LOCATION: (1377)
OTHER INFORMATION: n equals a,t,g, or FRATURE:
NAME/KEY: SITE
LOCATION: (1419)
COTHER INFORMATION: n equals a,t,g, or US-09-227-357-119 5 ACATAACCAAAAACGCATATGATT 28 EARLIER FILING DATE: 1997-09-12 STRANDEDNESS: single nucleic acid Query Match Best Local Similarity Matches 20; Conserva linear ; TOPOLOGY: lir; MOLECULE TYPE: US-08-139-937-12 ઠે

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Search completed: May 26, 2004, 17:56:36
Job time: 52.6325 secs
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Patent No. 5710022
GENERAL INFORMATION:
APPLICANT: Zhu, Wen-Hwa
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US93-11310-12/c
| Sequence 12, Application PC/TUS9311310
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: RELINDBLASTONA-ASSOCIATED PROTEINS
| TITLE OF INVENTION: RETINDBLASTONA-ASSOCIATED PROTEINS
| NUMBER OF SEQUENCES: A HT CORRESPONDENCE ADDRESS:
| ACRESPONDENCE ADDRESS:
| STREET: 4370 LA JOLLA VILLAGE DRIVE
| STREET: 4370 LA JOLLA VILLAGE DRIVE
| STREET: CALIFORNIA
| COUNTRY: USA
| COUNTRY: USA
| STREET: SALIFORNIA
| COUNTRY: USA
                                                                                             ö
Query Match 62.9%; Score 17.6; DB 1; Length 4868; Best Local Similarity 83.3%; Pred. No. 1.3e+02; Matches 20; Conservative 0; Mismatches 4; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US.

COUNTRY: US.

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11310
FILING DATE: 19-NOV-1993
CLASSIPICATION NUMBER: PCT/US93/11310
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: FP-CJ 9790
TELEPAN: 619-535-9001
TELEFAX: 619-535-9001
TELEFAX: 619-535-9001
TELEFAX: 619-535-9001
TELEFAX: GL9-535-9001
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                  4689 AACACATACCCACACACATATG 4666
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STATE: California
COUNTRY: USA
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US-08-328-254-5/c
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COMPUTER: POLICY
COMPUTER: PARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-CJ 1191
TELERDANE: (619) 535-9001
TELERDANE: (619) 535-9001
TELERDANE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 0789 base pairs
TYPE: MOLGAL Cacid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
62.9%; Score 17.6; DB 1;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8590 AACACATACCCACACACATATG 8567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 544..7990
US-08-328-254-5
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Sequence 3, Appli
Sequence 412, App
Sequence 7, Appli
Sequence 11, Appli
Sequence 166036,
Sequence 2014, App
Sequence 2014, Appli
Sequence 58, Appli
Sequence 61, Appli
Sequence 61, Appli
Sequence 61, Appli
Sequence 2286, Appli
Sequence 10855, Appli
                                                          May 26, 2004, 17:50:29; Search time 574.838 Seconds (without alignments) 221:574 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-222-952A-4
US-10-222-952A-3
US-10-222-952A-3
US-10-222-952A-7
US-10-222-952A-7
US-10-222-952A-7
US-10-22-952A-7
US-10-23-952A-7
US-10-175-523-6
US-10-175-523-7
US-10-175-523-7
US-10-175-523-7
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                    US-10-676-299-4:
28
E caacacataaccaaaacgcatatgatt 28
                                                                                                                                                                             2960401 segs, 2274450654 residues
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                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        - nucleic search, using sw model
                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                      Title:
Perfect score:
Sequence:
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21.6
21.6
21
20.6
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19.8
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No.
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Sequence 715, App
Sequence 1644, Ap
Sequence 204483,
Sequence 204483,
Sequence 129002,
Sequence 129002,
Sequence 260729,
Sequence 260729,
Sequence 9, Appli
Sequence 9, Appli
Sequence 107, App
Sequence 107, App
Sequence 1733, Ap
Sequence 7538, A
Sequence 320570,
Sequence 320570,
Sequence 7538, A
Sequence 320570,
Sequence 7641, A
Sequence 320571,
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US-10-22-952A-4

i Sequence 4, Application US/1022952A

i Sequence 4, Application US/1022952A

i CHAPLICATION NO. US20030096275A1

i GENERAL INFORMATION:

A PPLICANT: Laing Lance:

I TILLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES

FILE REFERENCE: 4107/11443-US;

FILE REFERENCE: 4107/11443-US;

FULE REFERENCE: 4007/11443-US;

PRIOR APPLICATION NUMBER: US/10/22,952A

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US 60/313,714

PRIOR PILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

ILENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: FRANTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: PLASLIB bottom, long oligo sequence
US-10-222-952A-4
US-10-311-455-715
US-10-087-192-1624
US-10-007-632-204483
US-10-027-632-204483
US-10-027-632-204483
US-10-027-632-129002
US-10-027-632-129002
US-10-027-632-260729
US-10-027-632-260729
US-10-027-632-260729
US-10-221-714A-501
US-10-221-75886
US-10-221-75886
US-10-027-632-75886
US-10-027-632-75886
US-10-027-632-75886
US-10-027-632-75886
US-10-027-632-75886
US-10-027-632-75889
US-10-027-632-32670
US-10-027-632-32670
US-10-027-632-32670
US-10-027-632-347688
US-10-027-632-47688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 28; DB 15
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 28; Conservative 0; Mismatches
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US-10-222-952A-3/c
'Sequence 3, Application US/1022952A
'Publication No. US20030096275A1
'GENERAL INFORMATION:
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US-10-240-453-11/c
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APPLICANT: Regenesis
APPLICANT: Laing, Lance
TITLE OF INVENTION: BLOOFINGS FOR SMALL MOLECULE ANALYTES
TITLE OF INVENTION: BLOO//1L443-US1
CURRENT FILID DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 30
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| Sequence 412, Application US/10087192
| Publication No. US20020182586A1
| GENERAL INFORMATION:
| APPLICANT: Boriel No. Eric K. | TILLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVELS: 2002-03-01 | PRIOR PILING DATE: 2002-03-01 | PRIOR APPLICATION NUMBER: US 09/747,377 | PRIOR PILING DATE: 2000-12-22 | PRIOR PILING DATE: 2000-02-03 | PRIOR FILING DATE: 2001-03-02 | NUMBER OF SEQ ID NOS: 2069 | SOFTWARE: PastSEQ for Windows Version 4.0 | SEQ ID NO 412 | MINDER OF MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF SEQ ID NO 412 | MIND APPLICATION NUMBER OF
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NAME/KEY: misc feature
LOCATION: (1)...(79860)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Artificial Seguence
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ORGANISM: Homo sapiens
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US-10-087-192-412
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US-10-222-952A-8
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APPLICANT: Regenesis APPLICANT: Laing, Lance TITLE OF INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES

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Sequence 11, Application US/10240453
Sequence 11, Application US/10240453
Publication No. US2030148326A1
GENERAL INFORMATION:
APPLICANT: PIEPERNBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Dy Means of Assessing the Methylation Status of Genes Associate
TITLE OF INVENTION: With DNA TRANSCRIPTION
TITLE OF INVENTION: WITH TRANSCRIPTION
TITLE OF INVENTION: WITH DNA TRANSCRIPTION
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US-10-222-952A-7
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Sequence 7, Application US/1022952A

Publication No. US20030096275A1

GENERAL INFORMATION:

APPLICANT: Regeneesis

APPLICANT: Laing, Lance

TITLE OF INVANTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES

TITLE OF INVANTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES

TILE REPERENCE: 4107/11443-US1

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US/10/222,952A

CURRENT FILING DATE: 2001-08-20

NUMBER: PRIOR PILING DATE: 2001-08-20

NUMBER: PRIOR PILING DATE: 2001-08-20

SOFTWARE: Patentin version 3.1

SEQ ID NO 7

LEMPIN: 23

LEMPIN: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.0%; Score 21; DB 15; Best Local Similarity 100.0%; Pred. No. 59; Matches 21; Conservative 0; Mismatches 0
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CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR PPLICATION NUMBER: US 60/313,714
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 21
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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SCHEACAL INCURCATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10887.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/0218,006

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/198,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-24

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-00-38

PRIOR PILING DATE: 1990-00-38

PRIOR
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82.1%; Pred. No. 2.8e+02;
tive 0; Mismatches 5; Indels
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/147,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/799,586
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-02-02
SOFTWARE PILING DATE: 2001-03-02
SOFTWARE PELNG DATE: 2001-03-02
SOFTWARE PELNG FOR WINDOWS VERSION 4.0
SEQ ID NO 2014
LENGTH: 248436
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| IOCATION: (1)...(246436)

| OTHER INFORMATION: n = A,T,C or G

US-10-087-192-2014
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Best Local Similarity 82.1
Matches 23; Conservative
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US-10-087-192-2014/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Human
US-10-027-632-166036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM:
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US-Gquence 166036, Application US/10027632

Publication No. US20020198371A1

GGENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FITLE OF INVENTION: LOGOTOLOGY, 632

CURRENT PILING DATE: 2002-04-30

CURRENT TLING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.6%; Score 20.6; DB 15; Length 6391; Best Local Similarity 85.2%; Pred. No. 2.3e+02; Matches 23; Conservative 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 CAAAACAAAACAAAAAACTCATGTGATT 302
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PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 11
LENGTH: 6391
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US-10-027-632-166036
; Sequence 166036, Application US/10027632
; Publication No. US200330204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Human
US-10-027-632-166036
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Gaps

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Sequence 2280, Application US/10349143
Publication No. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Evans, David
APPLICANT: Hook, Derek
APPLICANT: Hook, Derek
APPLICANT: Laeng, Pascal
APPLICANT: Laeng, Pascal
APPLICANT: Palireyman, Michael
APPLICANT: Rajan, Prith, Michael
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REPERENCE: 2323/14799-1433
CURRENT APPLICATION NUMBER: US/10/175,523
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                        Length 251364;
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Pred. No. 9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                    Query Match
70.7%; Score 19.8; DB 1
Best Local Similarity 91.3%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/299, 151
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR PLING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/315, 150
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-18
PRIOR FILING DATE: 2001-18
PRIOR FILING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
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; Publication No. US20030096264A1
; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 61
LENGTH: 251364
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Best Local Similarity 91.3%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Brockman, Jeffrey
                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Mus musculus
US-10-175-523-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-10-175-523-79
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US-10-349-143-2280/c
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                                                                                                                                                                                                                                                        APPLICANT: BY EVANGA, Delirey
APPLICANT: Hock, Derek
APPLICANT: Hock, Derek
APPLICANT: Hock, Derek
APPLICANT: Rijacak, Leszek
APPLICANT: Rijacak, Leszek
APPLICANT: Rijacak, Leszek
APPLICANT: Rijac, Pitch
APPLICANTON WINGER: US/10/175,523
CURRENT APPLICATION NUMBER: US 60/299,151
PRIOR FILING DATE: 2001-06-18
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2002-01-18
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Publication No. US20030096264A1
GARDRAL INPORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: However, Leszek
APPLICANT: However, Leszek
APPLICANT: Palfeyman, Michael
AAPLICANT: Bajan, Prithi
TITLE OF INVENTION: WULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REPRESENCE: 2225/10795-US3
CURRENT APPLICATION WUMBER: US 60/299,151
PRIOR PELING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR PLING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR PLING DATE: 2001-11-14
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                                                                                                                                        Sequence 59, Application US/10175523 Publication No. US20330096264A1 GENERAL INFORMATION: APPLICANT: Brockman, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Mus musculus
US-10-175-523-58
                                                                                                   -10-175-523-58/c
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US-10-175-523-61/c
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Query Match Best Local S Matches 21

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Gaps

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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-715
                                                                                                                                                                                                                                                                                                                                                                                                     Length 8087;
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                                                                                                                                                                                                                                                                                                                                                                                                     / Match 68.6%; Score 19.2; DB 15; Local Similarity 87.5%; Pred. No. 8.7e+02; Nes 21; Conservative 0; Mismatches 3;
                  PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
: SEQ ID NO 715
LENGTH: 8087
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Job time : 578.838 secs
  2002-12-16
                                                                                                                                                                                                                                                        TYPB: DNA ORGANISM: Artificial Sequence
  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Publication No. US20030143606A1
GRERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPERMRNOCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
FILE REPERMCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
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                  CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT APPLICATION NUMBER: US/09/422,978
PRIOR PILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
LENGTH: 47
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Fatent No. US2002013237A1
GENERAL INPORATION:
APPLICANT: Adjate, Paul A.
APPLICANT: Jones, Robert
FIGHERAL HATLOCKET, Susan L.
TITLE OF INVENTION: COMPOSITIONS NO METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPREENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT PILLIG DATE: 2001.05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: PastSEQ for Windows Version 4.0
ENGTH: 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 68.6%; Score 19.2; DB 16; Length 47; Best Local Similarity 80.8%; Pred. No. 3.5e+02; Matches 21; Conservative 1; Mismatches 4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: 99-10146-202 : polymorphic base T or A US-10-349-143-2260
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GENSET, 020CP1
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
COGANISM: Homo sapien
US-09-867-701-10855
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US-09-867-701-10855/c
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: allele
LOCATION: 24
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US-10-311-455-715/c
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

May 26, 2004, 15:22:28; Search time 299.923 Seconds (without alignments) 594.900 Million cell updates/sec

Run on:

US-10-676-299-5 Title: Perfect score:

1 ctgcacttacacattcgtta......tcatatatgtttttgactta 42 Sequence:

Gapop 10.0 , Gapext 1.0 Scoring table:

6747726 Fotal number of hits satisfying chosen parameters:

residues

3373863 segs, 2124099041

Searched:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_29Jan04:\* Database

geneseqn2001as:\* geneseqn2003as:\* geneseqn2003bs:\* genesegn1980s:\* genesegn1990s:\* geneseqn2003cs: geneseqn2000s:\* geneseqn2002s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseon2004s:\*

.. 30

# SUMMARIES

Description	Acd28586 B. coli A	Pro	Aas82555 DNA encod	Acd28587 E. coli A	Acd28591 E. coli A	Acd28590 E. coli A	Ada02963 Mouse Lck	Adb72701 Mouse Lck	Adc85443 Mouse Lck	Human	Abl21302 Drosophil	Abl18112 Drosophil	Abl05632 Drosophil	Abg71197 Listeria	Abg71020 Listeria	Abl11816 Drosophil	Aca49596 Prokaryot	Aag04704 USP-Promo	Abz17501 Arabidops	Abl15396 Drosophil	Abl05790 Drosophil	Abl05792 Drosophil	Abl04626 Drosophil
ID	ACD28586	ACA15469	AAS82555	ACD28587	ACD28591	ACD28590	ADA02963	ADB72701	ADC85443	ABN25854	ABL21302	ABL18112	ABL05632	ABQ71197	ABQ71020	ABL11816	ACA49596	AAQ04704	ABZ17501	ABL15396	ABL05790	ABL05792	ABL04626
DB	00	~	S	60	æ	œ	œ	σ	Q	9	4	4	4,	9	9	4	~	~	φ	4	4	4	4
Length	42	401	2182	40	25	25	29956	29956	29956	396	3503	6872	3109	1773	8148	3647	1146	1166	2000	3431	3741	3856	5082
% Query Match	200.0	300.0	100.0	95.2	59.5	59.5	55.7	55.7	55.7	54.3	53.8	53.8	53.3	52.9	52.9	52.4	51.9	51.9	51.9	51.9	51.9	51.9	51.9
Score	42	42	42	40	25	25	23.4	23.4	23.4	22.8	22.6	22.6	22.4	22.2	22.2	22	21.8	21.8	21.8	21.8	21.8	21.8	21.8
Result No.		7	е	Ω 4	S.	9	7	₩	σ	c 10	c 11	12	c 13	C 14	15	c 16	17	18	C 13	o 20	21	22	23

	Abi34061 Human ımm Abk31493 Signal tr
ABL29332 ABL29346 ABL19178 ABL19178 ABL34146 ABL34146 ABC34163 ABC21635 ABC216409 ABC816938 ABC816938 ABC816938	ABL34061 ABK31493
4 4 4 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0	φφ
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0.0.0.0.4.4.4.0.0.0.0.0.0.0.0.0.0.0.0.0	υ'n
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	200
121111111111111111111111111111111111111	21.2
4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 70
0000 0000 00	0.0

#### ALIGNMENTS

BP ACD28586 standard; DNA; 42 (first entry) L0-OCT-2003 ACD28586; RESULT 1 ACD28586 

B. coli Arsk binding oligonucleotide CHROMLIT.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003.

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

(LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specifically binds the bound specifically by the protein, and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the areance resistance operno of E. coll) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (5) inhibiting cellular proliferation or the activity of a gene in an operon required for poliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in equired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation, or the biological pathway in which a proliferation-required gene or its gene product lies
sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligonucleotide which binds to a chromosomally expressed ArsR protein and is used in the biosensor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screfor homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; ss; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prokaryotic essential gene antisense oligonucleotide #3339.
                                                                                                                                           Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen KL,
Forsyth RA,
                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                 CTGCACTTACACTTTCGTTTAAGTCATATATGTTTTTTGACTTA 42
                                                                                                                                                                                                            1 CIGCACITACACATICGITAAGICATAIATGITITITGACITA 42
                                                                                                       Sequence 42 BP; 11 A; 8 C; 5 G; 18 T; 0 U; 0 Other;
                                                                                                                                                        8.1e-06;
                                                                                                                                           DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R,
Yamamoto R,
                                                                                                                                                                           0; Mismatches
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                                                                                                                                         Score 42;
Pred. No.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                     ACA15469 Btandard; DNA; 401 BP.
                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923F.
; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                             42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-029926/02.
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-2003
19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002
                                                                       invention
                                                                                                                                                                                                                                                                                                                                                                       ACA15469;
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or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational culd discovery profiferation in cells other than S. aureus, S. typhimurium, C. Threumoniae or P. aeruginosa. The present sequence is one of the 513 cantisense sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained the constant of the contract of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 42; DB 7; Length 401; 100.0%; Pred. No. 1e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   Sequence 401 BP; 113 A; 68 C; 101 G; 119 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #18359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 18359; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS82555 standard; cDNA; 2182 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-PEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
P-PSDB; ABG18368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fomo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
        8888888888888888888888888888888
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useful for generating antibodies against it, detecting or quantitating a bolypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensize, gene mapping, identification of mutations and to produce other types of deta and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPD at fitp.wipo.int/pub/published_pct_sequences
     states involving (II).
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2182 BP; 516 A; 569 C; 582 G; 515 T; 0 U; 0 Other;
  disease
     to treat
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Gaps
                                 ö
100.0%; Score 42; DB 5; Length 2182;
100.0%; Pred. No. 1.2e-05;
iive 0; Mismatches 0; Indels (
                Local Similarity 100.
   Query Match
                                Matches
```

# 487 CTGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 528 42

셤

ACD28587 standard; DNA; 40 ACD28587;

10-OCT-2003 (first entry)

B. coli ArsR binding oligonucleotide CHROMLIB.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003.

15-AUG-2002; 2002US-00222952

20-AUG-2001; 2001US-0313714P

(LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English

The invention relates to a new system (blosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the arsenic resistance operno of B. coll) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid 

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sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds to a chromosomally expressed ArsR protein and is used in the biosensor of
  8888888
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Sequence 40 BP; 17 A; 5 C; 7 G; 11 T; 0 U; 0 Other;

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Gaps
                               ö
       Score 40; DB 8; Length 40;
Pred. No. 4.2e-05;
                              0; Indels
95.2%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                  Local Similarity 100.
Les 40; Conservative
       Query Match
                               Matches
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42

3 GCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 40 GCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA

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ACD28591 standard; DNA; 25 BP RESULT 5 ACD28591/c

ACD28591;

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(first entry) 0-0CT-2003 E. coli Arsk binding oligonucleotide CHROMSIB.

ArsR; arsenic resistance operon; biosensor; 8s; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

(LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and mucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein, and specific binding sequence that is bound specifically by the protein, and containing a specific binding sequence that is bound specifically by the protein and sequence of the analyte. Also included are biosensor device for detecting the presence of an analyte in a sample, and an Arsk (encoded by part of the arsenic resistance operon of E. coli) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as ABUGA440 binding to a nucleic acid sequence comprising oligonucleotides appearing as ACD28581. The system is useful for detecting the presence of analyte in a sample. The system is useful for detecting the presence of analyte in a sample. The presence is the bottom strand of an oligonucleotide which binds to a chromosomally expressed Arsk protein and is used in the biosensor of the invention

Sequence 25 BP; 13 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

DB 8; Length 25; 10; Score 25; Pred. No. 59.5%; S 100.0%; Query Match Best Local Similarity

ઠે 셤 Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;

26-DEC-2002; 2002WO-US041414. 26-DEC-2001; 2001US-00035832.

WO2003057146-A2,

17-JUL-2003

(SAGR-) SAGRES DISCOVERY

WPI; 2003-587068/55.

Worris DW;

carcinoma associated gene, SEQ ID NO:1481.

06-NOV-2003 (first entry)

ADA02963;

Mouse Lck

gene; ds.

Mus sp.

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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein; to the nucleic acid in the presence of the analyte. Also included are a consensor device for detecting the presence of an analyte in a sample, and an Arsk (encoded by part of the arsenic resistance operon of E. coll) protein comprising an min acid sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as Aud28584-ACD28591. The sequence comprising oligomucleotides appearing as AUD28584-ACD28591. The present sequence is the top strand of an oligomucleotide which binds to a chromosomally expressed Arsk protein and is used in the biosensor of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the mucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.
       Gaps
       ..
0
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArsR; arsenic resistance operon; biosensor; ss; arsenic.
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       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. coli ArsR binding oligonucleotide CHROMSIT.
   Mismatches
                                                                  4
                                                                                                      25 TTAAGTCATATATGTTTTTGACTTA 1
                                                                  TITGACTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 35; Page 15; 36pp; English.
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                                                                                                                                                                                                                                                                                             ACD28590 standard; DNA; 25 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
25; Conservative
                                                               18 TTAAGTCATATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-576876/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LAIN/) LAING L G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003096275-A1.
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                                                                                                                                                                                                                                                                                                                                                                ACD28590;
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Matches
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New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.

Claim 1; SEQ ID NO 1481; 245pp; English.

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                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                    Sequence 29956 BP; 6634 A; 6708 C; 6677 G; 7953 T; 0 U; 1984 Other;
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                                                                                                                                                                                                                                                                                                                              23.4; DB 8; Length 29956;
No. 79;
                                                                                                                                                                                                                                                                                                                              Query Match 55.7%; Score 23.4; DB 8; Length 2 Best Local Similarity 73.2%; Pred. No. 79; Matches 30; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                              18517 CIGCAITCATTCATTCATTCATTCATATTTTGATTT 18557
                                                                                                                                                                                                                                                                                                                                                      1 CTGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTT 41
                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                             g
G
                                                                                                                                                                                                                                                                                                                                                                                            ADB72701 standard; DNA; 29956
                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2003
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Gaps

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59.5%; Score 25; DB 8; Length 25; 100.0%; Pred. No. 10; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 25; Conservative

TIAAGICATATATGTTTTTGACTIA 42

18

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TTAAGTCATATATGTTTTTGACTTA

RESULT 7 ADA02963 ID ADA02963 standard; DNA; 29956 BP.

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directly from WIPO at

n electronic

The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. Them. The invention also encompasses expression vectors and host calls comprising a invention also encompasses expression vectors and host calls comprising to invention also encompasses expression vectors and host calls comprising to binds to the protein, and a blochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using a random. Many of these do not carry transduced host oncogenes or a random. Many of these do not carry transduced host oncogenes or pathogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic variant genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host carcinoma (especially breast cancer, prostate cancer, lymphoma or the propersion of the sequence of the sequence of the invention of CA gene expression in particular crissues. CA mucleic acids, proteins and antibodies are also useful as thermeuter sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this entering from a properial very from a properial very from a properial very from a protein and evaluation, but was obtained in alertronic forms a specifical as protein and evaluation.

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f rou way 2/ IU:II:42 2004
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The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polyneptices are useful for treating carcinomas, e.g. lymphomas, cancers, neopleam, adenocarcinoma, and sarcommas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                               mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29956 BP; 6634 A; 6708 C; 6677 G; 7953 T; 0 U; 1984 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 9; Length 2 Pred. No. 79; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 529; 2304pp; English
                                                                                                                                                                                                                            02-MAR-2001; 2001US-00798586.
23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00034650.
                                                                                                                                                                                                26-DEC-2001; 2001WO-US051291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 55.7%;
Best Local Similarity 73.2%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                  Engelhard EK;
                                                                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-239337/23
                                                                                                                             WO2003008583-A2
                                                                                                                                                                30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                  DY,
                                             mouse;
                                                                                                                                                                                                                                                                                                                                                                  Morris
                                                                                               Mus sp
                 Mouse
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ö Gaps .. 29956; 18517 CTGCATTCATTCATTCATTCATTCATATTTTGATTT 18557 셤

ADC85443 standard; DNA; 29956 BP Mouse Lck genomic sequence (first entry) 01-JAN-2004 ADC85443; 

Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; secreted; transmembrane; intracellular; ds.

Mus sp

WO2003045230-A2

05-JUN-2003

02-DEC-2002; 2002WO-US038582

30-NOV-2001; 2001US-00997722

(SAGR-) SAGRES DISCOVERY.

Morris DW, Engelhard EK;

οę New recombinant nucleic acid comprising a nucleotide sequence of any the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.

The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention. 

Sequence 29956 BP; 6634 A; 6707 C; 6677 G; 7953 T; 0 U; 1985 Other;

Gaps ô 11; Indels Query Match Best Local Similarity Matches

18517 CTGCATTCATTCATTCATTCATTCATATTTTTTCATTT 18557 à 셤

Human ORFX polymuclectide sequence SEQ ID NO:20185.

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyrodism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis; gene; ss. 

Disclosure, SEQ ID NO 20185; 1037pp; English

ms-rn-e/e-zaa-orma

WPI; 2003-513603/48.

Claim 1; SEQ ID NO 229; 983pp; English.

DB 9; Length 29956; ch 55.7%; Score 23.4; D Similarity 73.2%; Pred. No. 79; 30; Conservative 0; Mismatches

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1 CIGCACITACACATTCGTTAAGTCATATATGTTTTTGACTT 41

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Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

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The present investines suppositions build that the specification). ABNIS762 to ABNIS752 encode the human ORFX proteins are useful for in the specification). ABNIS762 to ABNIS752 encode the human ORFX proteins given in ABNIS762 to ABNIS752 encode the human ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the creatment of cancer, hyperproliferative disorders, cirrhosts of liver, psoriasis, benign tumours, Reloid, degenerative disorders related to organ cransis, benign tumours, Reloid, degenerative disorders related to organ cransplantation, cardiovascular disease, disorders, infectious systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune disorders and disorders, infectious disease, autoimmune thyroiditis, mysthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also carthritis, autoimmune inflammatory eye disease. ORFX proteins are also bone degenerative disorders, increasing organic consist.

Conseful for treating burns, incisions, ulcers, for treating osteoporosis, correction or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
              present invention describes substantially purified human proteins Parred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polymucleotide SEQ ID NO 15379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%; Score 22.8; DB 6; Length 396; 79.4%; Pred. No. 85; ive 0; Mismatches 7; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 396 BP; 148 A; 81 C; 51 G; 116 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 TTACACATTTGTAAAGACAAAAATGTTATTAACT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TIACACATTCGTTAAGTCATATATGTTTTGACT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB121302 standard; DNA; 3503 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 79.4
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical fungs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-BB12017). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide; cal; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 5809.
                                                                                                                                                                                                                                                    / Match 53.8%; Score 22.6; DB 4; Length 3503; Local Similarity 75.7%; Pred. No. 1.2e+02; les 28; Conservative 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6872;
                                                                                                                                                                                                                   Sequence 3503 BP; 1061 A; 740 C; 725 G; 977 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 5809; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                         948 reracaracacarirergaarrerrrrrrrrraa 912
                                                                                                                                                                                                                                                                                                                                     2 TGCACTTACACATTCGTTAAGTCATATATGTTTTGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22.6; DB 4;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL18112 standard; DNA; 6872 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US009231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmer
pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adame M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL18112;
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                                                                                                                                                                                                                                                                                 Best Loc
Matches
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The present invention relates to nucleic acid sequences (ABQ67188-ABQ7212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to serien for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at Etp. wipo.inf/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                           Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial, Listeria, food contamination; mutational analysis; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1773 BP; 624 A; 223 C; 340 G; 537 T; 0 U; 49 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes 4b contig DNA sequence #962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22.2; DB 6;
Pred. No. 1.6e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1230 receraceacarrecriragierecegarerrir 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCACTTACACATTCGTTAAGTCATATATGTTTTT 36
                                                  Listeria monocytogenes 4b specific contig124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; SEQ ID NO 4010; 180pp; French.
                                                                                                                                                                     Listeria monocytogenes ATCC 19115
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                                                                                                                                                                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                              04-OCT-2001; 2001WO-FR003061.
                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000; 2000FR-00012697.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.9%;
Best Local Similarity 77.1%;
Matches 27; Conservative
  29-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-332479/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunst F, Glaser P;
                                                                                                                                                                                                                WO200228891-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40200228891-A2
                                                                                                                       infection; ds.
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29-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of disciolas, therapeutics and pharmaceutical frugs. The invention disciolase genomic DNA sequences (ABL15176-ABL30511), expressed DNA ABB12012). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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  Gaps
                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 11378.
                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 11378; 21pp + Sequence Listing; English.
  Indels
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Pred. No. 1.4e+02;
0; Mismatches 11
  Mismatches
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                                                                                                                                                                                                                ABL05632 standard; cDNA; 3109 BP.
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                                                                                                                                                                                                                                                                                                              26-MAR-2002 (first entry)
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hes 29; Conservative
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
P-PSDB; ABB61529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001.
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ABQ71197/c
ID ABQ71115
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AC ABQ71115
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DT 29-AUG-
  Matches
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RESULT 13
ABLOS 22/1
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Length 1773;

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The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to sorien for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                         New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 8148 BP; 2408 A; 1730 C; 1229 G; 2781 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.9%; Score 22.2; DB 6; Length 8148; Best Local Similarity 77.1%; Pred. No. 1.96+02; Matches 27; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                        Claim 14; SEQ ID NO 3833; 180pp; French.
                                                                                                          (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                   04-OCT-2001; 2001WO-FR003061.
                                                                04-OCT-2000; 2000FR-00012697.
                                                                                                                                                                                                                             WPI; 2002-332479/37.
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Gaps

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Search completed: May 26, 2004, 17:50:05 Job time : 303.923 secs

us-10-676-299-5.rni

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APPLICANT: Casell, Gail H.
APPLICANT: Casell, Gail H.
APPLICANT: Chen, Elleon Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: UVCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: URBALT/TICUM
TITLE OF INVENTION: UNCALT/TICUM
TITLE OF INVENTION: URBALT/TICUM
TITLE OF INVENTION: UNCALT/TICUM
TITLE OF INVENTION UNBER: US/09/601,198
CURRENT FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
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                                                                                                                                May 26, 2004, 16:18:00 , Search time 66.9487 Seconds (without alignments)
348.146 Million cell updates/sec
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1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-601-198-111
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US-09-541-681A-1066
US-09-499-203-15
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US-09-499-203-16
US-09-499-203-17
US-09-499-203-17
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US-09-426-290-1
US-09-426-290-1
US-09-328-352-1636
US-09-60-312D-572
US-09-613-394A-4
US-09-613-137-1
US-09-52-137-1
US-09-53-137-1
US-09-543-681A-376-1
US-09-543-650A-20
US-09-543-453-35-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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Sequence 1096, Application US/09134001C
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79, Appl
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112, Appl
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603, App
7058, Ap
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1407, Appl
16107, Appl
16108, Appl
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US-09-134-001C-603
US-09-134-01C-603
US-09-135-1327
US-09-671-125-1327
US-09-671-325-1327
US-09-621-976-46107
US-08-96-959-1
US-08-96-959-1
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US-09-430-497A-8
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US-09-601-198-111/c
Sequence 111, Application US/09601198
; Patent No. 6531583
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NS-09-708-725A-3/C

Sequence 3, Application US/09708725A

Sequence 3, Application US/09708725A

Sequence 3, Application US/09708725A

Sequence 3, Application US/09708725A

TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: UNMBER: US/09/708,725A

CURRENT APPLICATION NUMBER: 60/243,428

PRIOR FILLING DATE: 2000-10-27

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 3

LENGTH: 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09499203
| Sequence 16, Application US/09499203
| Patent No. 657065
| Fatent No. 657065
| Fatent No. 657065
| APPLICANT: WELSH, Thomas
| APPLICANT: WINTH, KATONA
| APPLICANT: WOUNTH, KATONA
| TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase
| TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase
| CURRENT FILING DATE: 2000-02-08
| NUMBER OF SEQ ID NOS: 54
| SOFTWARE: Patentin Ver. 2.1
| SEC ID NO 16
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APPLICANT: KOSSMANN, Jens
APPLICANT: QUANZ, MALIN
APPLICANT: RAUTH, Karola
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternangucrase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.5%; Score 20.8; Di
70.0%; Pred. No. 70;
rative 0; Mismatches
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CRGANISM: Leuconostoc mesenteroides
US-09-499-203-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 70.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Human
US-09-708-725A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-499-203-16/c
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Fatent No. 6605709
GRANKAL INFORMATION:
APPLICANT: GARY ERETON
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TOWNERNT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1066
LENGTH: 1275
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Fatent No. 6570065
GENERAL INFORMATION:
APPLICANT: KOSSMANN, Jens
APPLICANT: WEISH, Thomas
APPLICANT: WISH, Marcin
APPLICANT: KNUTH, Karcin
APPLICANT: KNUTH, Karcin
APPLICANT: KNUTH, Karcin
APPLICANT: KNUTH, Karcin
CURLENT: RAPPLICANT: WISHERS: US/09/499,203
CURRENT APPLICATION NUMBER: US/09/499,203
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Solo8; Score 21; DB 4; Length 711;
Best Local Similarity 82.88; Pred. No. 53;
Matches 24; Conservative 0; Mismatches 5; Indele
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49.5%; Score 20.8; DB 4; Best Local Similarity 70.0%; Pred. No. 69;
Matches 28; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                  74 ATTGGTTGAGTCACATATGATT 46
                                                                                                                                                                                                                                                                                                   13 ATTCGTTAAGTCATATATGTTTTTGACTT 41
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                                                                                ; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 73.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Proteus mirabilis
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 111
LENGTH: 711
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SEQ ID NO 15
LENGTH: 1917
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APPLICANT: WELSH, Thomas
APPLICANT: WELSH, Thomas
APPLICANT: WELSH, Thomas
APPLICANT: WINTH, Martin
APPLICANT: KNUTH, KAICH
TITLE OF INVENTION: Nucleic Acid Molecules Encocing Alternangucrase
FILE REPERSINCE: 147-196P
CURRENT APPLICATION UNDERS: US/09/499,203
CURRENT APPLICATION UNDERS: 194
SUFTHARE OF SEQ ID NOS: 54
SSOTHARE: PALENTH VET. 2.1
LENGTH: 9321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09499203
Fatent No. 6570065
GENERAL INFORMATION:
APPLICANT: KOSSMANN, Jens
APPLICANT: WELSH, Thomas
APPLICANT: KNUTH, Karola
APPLICANT: KNUTH, Karola
APPLICANT: GUNZ, Martin
APPLICANT: GNAVE, Martin
APPLICANT: WELSH, Thomas
APPLICANT: WELSH, Thomas
APPLICANT: WELSH, Thomas
APPLICANT: GNAVE, Martin
APPLICANT: NUTH, Earle
APPLICANT: NUTH, Earle
APPLICANT: Asrola
CURRENT APPLICANTON: NUCHEIC Acid Molecules Encoding Alternansucrase
CURRENT APPLICANTON: NUCHEIC ACID
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.1
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49.5%; Score 20.8; DB 4; Length 6204;
Best Local Similarity 70.0%; Pred. No. 78;
Matches 28; Conservative 0; Mismatches 12; Indels 0;
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Pred. No. 80;
0; Mismatches
FILE REPERENCE: 147-196P
CURRENT APPLICATION NUMBER: US/09/499,203
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 6204
                                                                                                                                                        TYPE: DNA

RCANISM: Leuconostoc mesenteroides
US-09-499-203-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Leuconostoc mesenteroides
US-09-499-203-17
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Patent No. 6570065
GENERAL INPORMATION:
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Best Local Similarity 70.0%;
Matches 28; Conservative
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; LOCATION: (678)..(6848)
US-09-499-203-1
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US-09-499-203-17/C
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SEQ ID NO 17
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Sequence 10, Application US/10027983
Sequence 10, Application US/10027983
Sequence 10, Application US/10027983
Sequence 10, Application US/10027983
Sequence 10, 6617162
SEQUENCEMENTION: Mark P. Roach
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECRPTOR ALPHA EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECRPTOR ALPHA EXPRESSION
CURRENT FILING DATE: 2011-12-18
SEQUENCEMENT OF SEQUENCE
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Pred. No. 96;
0; Mismatches 9; Indels 0
DB 4; Length 9321;
                                                                                     12; Indels
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Score 20.8; Di
Pred. No. 82;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: S'UTR
LOCATION: (1)...(2302)
NAME/KEY: exon:exon junction
LOCATION: (1491)...(1492)
OTHER INFORMATION: exon 4:exon 5
NAME/KEY: start codon
LOCATION: (2302)...(2305)
NAME/KEY: 3'UTR
LOCATION: (2735)...(8566)
NAME/KEY: exon:exon junction
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; OTHER INFORMATION: exon 11:exon 12
US-10-027-983-10
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OTHER INFORMATION: exon 10:exon 11
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OTHER INFORMATION: exon 8:exon 9
NAME/KEY: exon:exon junction
LOCATION: (3708)...(3709)
OTHER INFORMATION: exon 9:exon 10
NAME/KEY: exon:exon junction
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Best Local Similarity 74.3%;
Matches 26; Conservative
Query Match
Best Local Similarity 70.0%;
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-10-027-983-10/c
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US-09-426-290-1/c
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Gaps

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US-09-328-352-1636/c

Sequence 1636, Application US/09328352

Sequence 1636, Application US/09328352

Sequence 1636, Application US/09328352

Setting No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

APPLICANTION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT PAPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LEAVER OF SEQ ID NOS: 8252
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                                                                         DB 2; Length 342;
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                                                                    Score 20.4; DE Pred. No. 80; 0; Mismatches
                                                                                                                                                                       9 ACACATTCGTTAAGTCATATATGTTTTGA 38
                                                                                                                                                                                                                      14 ACACGINGGINAGICITATITAGITITICA 43
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PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-620-312D-572/c

: Sequence 572, Application US/09620312D

: Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA; CRGANISM: Acinetobacter baumannii
US-09-328-352-1636
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SOFTWARE: pt FL genes Version 1.0
SEQ ID NO 572
                                                                      Query Match
Best Local Similarity 80.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
Drmanac, Radoje T
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Asundi, Vinod
Zhang, Jie
Ren, Feiyan
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Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen, Rui-hong
Zhao, Qing A.
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Kue, Aidong J
; STRAIN: ATCC 27958
US-08-607-384A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 168575;
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APPLICANT: PORSNAN, P IVI TUULIKKI
APPLICANT: PISALA-TIMISJ RVI, ANU KYLLIKKI
TITILE OF INVENTION: DNA SEQUENCE-BASED DIAGNOSIS OF MASTITIS
TITLE OF INVENTION: FROM A MILK SAMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILILE OF INVENTION: FROM A MILK SAMFLES

NUMBERS OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSER: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER: ELOPPY disk

COMPUTER: ELOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PLOPPY disk

COMPUTER: 120 PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PLOPPY disk

CLASSIFICATION NUMBER: US/08/607,384A

FILING DATE: 27-FEB-1996

CLASSIFICATION: 435

ATTORNEY THOMAS B.

REGISTRATION NUMBER: 32,205

REGISTRATION INPORMATION:

NAME: BYRNE THOMAS THOMAS TOWN

TELECHOMUNICATION INPORMATION:

TELECHOMUNICATION INPORMATION:

TELECHOMUNICATION INPORMATION:

TELECHOMUNICATION INPORMATION:

TELECHOMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

Query Match

Best Local Similarity 74.3%; Pred. No. 1.3e+02;

Matches 26; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 TACACATTCGTTAAGTCATATATGTTTTTGACTTA 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....arhone: (703) 816-4000
TELEPAX: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
TENGTH: 342 herestrics:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                               (127009) ... (127130)
                                                                                                                                                                                                               (101753)...(101996)
                                                                                                                                                                                                                                                                   (110324)...(110439
                                                                                                                                                                                                                                                                                                                  (124058)...(124278
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                                                                                              CDS (21181)...(21403)
                                                                                                                                                                  (95252)...(95430)
                    TYPE: DNA
ORGANISM: Homo Sapiens
LENGTH: 168575
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                                                                                                                                                                                                                                                                                                                                                                                                              , LOCATION: (
US-09-426-290-1
                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
NAME/KEY:
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NAME/KEY:
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Gaps

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FESCULE 13-

FESCULE 13-

FESCULE 13-

FESCULE 143

FESCULE 15-

FESCULE 15-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1930 ACTGAAACATATAGTAAGTTATATATTTTTTAGATATA 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA
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APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION ENTREME: 05000,861
FILING DATE: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
APPLICATION NUMBER: 08/781,986
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKGT NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 443:
US-08-956-171E-443
                                                                                                                          | FEATURE:
| NAME/KEY: CDS
| FOATION: (202)..(1212)
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(2728)
| OTHER INFORMATION: n = a,t,c or g
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LENGTH: 5301 base pairs
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LENGTH: 2728
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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Searched:

Database

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Canis familiaris (dog)

Canis familiaris

Canis familiaris

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammaila; Eutheria; Carnivora; Pissipedia; Canidae; Canis.

1 (bases 1 to 502)

S O'Shaughnessy,A.L.; McCombie,W.R.; Baker,J.P.; Balija,V.;

Cunnius,D.; Dedhia,N.N.; Mela Bastide,M.; Katzenberger,F.;

King,L.; Kirchoff,K.A.; Miller,B.; Muller,S.; Nascimento,L.U.;

Pranter,L.; Santos,L.; Shah,R.S.; Spiegel,L.A.; Zutavern,T.;

Preston,R. and Hamnon,G.J.

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884

Fax: 516 367 8884
BE824180 GM700023A
CE456382 tigT-gss-
CE12602 tigT-gss-
CE212602 tigT-gss-
CE212602 tigT-gss-
BH74046 TOOS RPLP
CG231937 OGVDL6ZTV
CG231937 OGVDL6ZTV
CG1962590 PUTCM17TB
CG182580 PUTCM17TB
CG182590 PUTCM17TB
CG52118 PUTCM17TB
CG371624 MBRL23TF
BC429190 AGENCOURT
CG371624 MBRL23TF
BC429190 AGENCOURT
CG62616 PUTGT-gss-
CG08218 LigT-gss-
BZ178813 CH230-349
CG652813 PUTGW15GTB
CG652813 PUTGW15GTB
BB120824 BB120824
W89216 mg18807:r1
BF322026 uz52a04.x
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CD29226 StrPuts36.
BE032011 130801 MA
BH015678 TDGCD56TH
BH433034 BCHWY1TF
BH315621 CH230-12J
CC086257 CSU-K33r.
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  BBB34180
CE8496382
CE812602
BE2388776
BB1744046
BB1744046
CG211937
AZ405411
CG197578
BE061184
BE0611848
BC04200118
CG182590
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CE008178
CD082216
CG052813
CG966166
CG052815
BB120824
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CD292926
BE032011
BH015678
BH423034
BH315621
CC086257
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  RESULT 1
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LOCUS
DEFINITION
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XEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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BM307747 sak33d01.
AW458707 sh12f03.y
BM568294 sal02e04.
                                                                                       May 26, 2004, 16:21:09; Search time 2910.03 Seconds (without alignments) 430.997 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                            1 ctgcacttacacattcgtta.....tcatatatgtttttgactta
                                                                                                                                                                                                                                                                           55026578
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                               27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                   nucleic search, using sw model
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BM307747
AW458707
BM568294
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em_gss_vrl:*
gb_gssl:*
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em gss pln:
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Maximum DB seq length: 200000000
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2: em_esthum:*
3: em_esthum:*
5: em_estrov:*
6: em_estrov:*
7: em_estro:*
9: 9b_est1:*
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Match Length DB
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Perfect score:
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us-10-676-299-5.rst

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VERSION
KEYWORDS
SOURCE
ORGANISM
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AW458707
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/fissue type="testes"
/folome lib="Canis cDNAs from testes cells"
/note="Vector: lambda Zap II; The library was produced by
Greg Hannon and Raymond Preston (Cold Spring Harbor
Laboratory). This library is oligo(dT) primed using
strategene Zap CDNA synthesis kit. It was made from dog
testes. Please contact Greg Hannon (hannon@cshl.org) with
any library related inquiries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 bp mRNA linear EST 02-JAN-2002 sak33dd1.yl Gm-c1075 Glycine max cDNA clone SOYBRAN CLONE ID: BM307747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: {800}-533-4363 or contact: ccu@resgen.com web site:
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/db_xref="taxon:3847"
/clone="sOYBEAN CLONE ID: Gm-c1075-4777"
/clone="SOYBEAN CLONE ID: Gm-c1075-4777"
/clssue_type="differentiating somatic embryos cultered on MSMGAG"
/lab_host="DH10B"
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                                                                                          organism="Canis familiaris"
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Seq primer: -40RP from Gibco
High quality sequence stop: 223.
Location/Qualifiers
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Plate: hb05 row: c column: 02
Seg primer: -21M13Univ8rev
High quality sequence stop: 502.
Location/Qualifiers
                                                                                                          /mol_type="mRNA."
/db_xref="taxon:9615"
/clone="hb05c02"
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| Annual Processing Palescript IS Skr, Site 1: Ecoli, Site 2; Annual Processing Palescript IS Skr, Site 1: Ecoli, Site 2; Annual Processing Palescript IS Skr, Site 1: Ecoli, Site 2; Annual Processing Palescript IS Skr, Site 2; Annual Skr, Site 2; Annual Skr, Site 3; Annual Skr, Site 3;
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Xhol; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a Xhol restriction site. EcoRl adapters were ligated to the blunt-ended cDNA fragments followed by Xhol digestion. The CDNA fragments were directionally cloned into the EcoRl-Xhol restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. (bases 1 to 525)
Shoemaker,R., Keim,P., Vodkin,L., Brpelding,J., Coryell,V.,
Shoemaker,R., Keim,P., Vodkin,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Materston,R., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525 bp mRNA linear EST 21-FEB-2002 sallozed4.yl Gm-c1057 Glycine max cDNA clone SOYBEAN CLONE ID: EM568294
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South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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/note="Vector: pBluescript II SK+; Site 1: EcoRI, Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 2 week old seedlings from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Awashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                        59.0%; Score 24.8; DB 10; Length 481; 80.6%; Pred. No. 2.3e+02; Live 0; Mismatches 7; Indels 0;
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/mol_type="mRNA"
/db Zref="texon:3847"
/clone="SOYBBAN CLONE ID: Gn-c1057-4063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -40RP from Gibco
High quality sequence stop: 434.
Location/Qualifiers
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AUTHORS
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RESULT 4

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ORIGIN

PEATURES

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/....../
/ coganism="Glycine max"
/mol_type="mRNN"
/mol_type="mRNN"
/db xref="taxon:3847"
/clone="dm-r1070-8886"
/clone="m-r1070-8886"
/clone="m-r1070-8886"
/clone="m-r1070-8886"
/clone="mhe library Gm-r1070 is a sequence-driven, reracked set 0;9;18 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from young pods. The 5' ESTS of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to a representative of each contig, which were reracked form library Gm-r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by
P1469916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the BCORI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRI). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V.,
Brpelding, J., Raph, C., Shoop, B., Pardinas, J., Liu, L. and Lewin, H.
Bructional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Other ESTS: AN566322 corresponding to Gm-r1030-3256 (5')
Contact: Vodkin, L.O., Pl., A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional
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GM700023A20B3 Gm-r1070 Glycine max cDNA clone Gm-r1070-8886 3',
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
1217) 244-6147
Fax: (217) 334-4582
Email: 1-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Ganome Systems, Inc. 4633 World
Email: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.0%; Score 24.8; DB 12; Length 525; Best Local Similarity 80.6%; Pred. No. 2.3e+02; Matches 29; Conservative 0; Mismatches 7; Indels 0;
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Seq primer: 5'-TTTTTTTTTTTTTTTTTTTTTA (A/C/G)-3'.
Location/Qualifiers
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BE824180.1 GI:10256414
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Glycine max
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BE824180
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נוספ-33 bp DNA linear GSS 25-SEP-2003
tigr-gss-dog-17000371501174 Dog Library Canie familiaris genomic,
genomic survey sequence.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0206
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
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tigr-gss-dog-17000372765569 Dog Library Canis familiaris genomic,
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Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
1 (Dases 1 to 621)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Wenter, J.C.
                                                                                                                                                                                     Canis familiaris (dog)
Canis familiaris
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Canidae; Canis.
Mammalla; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 533)
1 (bases 1.c. 533)
Rusch, D.B., Deloher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
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/clone lib-"Hog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blocd"
                                                                                                                                                                                                                                                                                                                                                                         The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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CE195732.1 GI:35351385
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Canis familiaris
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the laboratory of Ernest Retzel, Center for Computational Genomics and Bloinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Scybean/index.html. Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Runctional Genomics, University of Illinois, the Minchest of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-11070 library is listed in the 'OTHER BST' field. The detailed information on the source library for each clone can also be obstained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 bp DNA linear GSS 28-SEP-2003
genomic survey sequence.
CE496382.
GSS 58-SEP-2003
CE496382.
GSS 58-SEP-2003
CE496382.1 GI:36813163
GSS.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (dog)
Canis familiaris
Canis familiaris
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 379)
1 (kases, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, M., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/clone_lib="Dog_Library"
/noto="Site_l: astXI; Libraries were prepared from
peripheral blood"
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                                                                                                                                                                                                                                                                                                                                                                         th 59.0%; Score 24.8; DB 10; Length 640; I Similarity 80.6%; Pred. No. 2.3e+02; 29; Conservative 0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.1%; Score 24.4; DB 29; Length 379; 73.8%; Pred. No. 3.1e+02; rive 0; Mismatches 11; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 TAATTCATTCGCTAAATCATATATATTTTCGACTTA 163
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/strain="Standard Poodle"
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Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Conservative
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CE496382/c
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BH174046 10064 bp DNA linear GSS 09-OCT-2001 T005 RFLP clone from soybean genomic DNA Glycine max genomic clone pT005, genomic survey sequence.
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                                                                                                                                                                                                                     Glýcine max (soybean)
Glýcine max
Glýcine max
Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 255)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budinan, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.1%; Score 24; DB 28; Length 1064; 75.0%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                  Glycine.

1 (bases 1 to 1064)
Grant, D. and Shoemaker, R.C.
unpublished sequence of soybean RFLP probe
Unpublished (2001)
Contact: Grant D
Agronomy Department D
Agronomy Department
Globel Agronomy Hall, Ames, IA 50011-1010, USA
Tel: 515 294 1205
Fax: 515 294 1205
Rax: 515 294 2299
Ramil: Agrant@iastate.edu
single pass sequence
Class: RFLP clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 CTGTCACTATATATAGTTAATTCATATATGTTTATGAAT 45
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                                 6 CITACACATICGITAAGICATATATGITITIGACTIA
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CG231937.1 GI:34131823
                                                                                                                                                                                       BH174046.1 GI:15989413
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Matches 30; Conserv
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BH174046/c
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                                                                                                                                  /clone lib="Dog Library"
/note="Site 1: BstXI, Libraries were prepared from
peripheral blood"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DRM was provided by Daniel Eichinger
Seg primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                       496 CIGCACATCCACATAAATIGAATCATATATGGTTTTTTATTA 455
                                                                                                                                                                                                                                                                                       1 CIGCACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 42
                                                              1. .621
/organism="Canis familiaris"
/mol_type="genomic DNA"
strain="Stendard Poodle"
/db_xref="taxon:9615"
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                                             Location/Qualifiers
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
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Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZ388776.1 GI:30235313
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Entamoeba invadens
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Matches 29; Conserv
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BZ388776
                                               FEATURES
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Gaps

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/mol_type="genomic DNA"
/strain="B73"
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1. 480
/organism="Zea mays"
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CG197578
CG197578.1 GI:34088639
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Other GSSs: PUFMC47TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: TF
Class: sheared ends
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Matches 29; Conservative
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CG197578
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Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ405411
1M0174A13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0174A13 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                              Gans
                                                                                                                                                                                                                     /mol_type="genomic DNA"
/stain="873"
/db xxef="taxon:4577"
/clone="ZxwEMMa0511K04"
/clone="lb="Zxy"
/clone="Vector: pBCSk-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                    56.2%; Score 23.6; DB 29; Length 255; llarity 76.3%; Pred. No. 5.9e+62; Conservative 0; Mismatches 9; Indels 0
           153 AATTATATATCATTAAGTAATATATGAATTTAATTTA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ACTTACACATTCGTTAAGTCATATATGTTTTTGACTTA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0174 row: A columm: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0174A13"
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/organism="Zea mays"
                                                                                                                         Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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Mus musculus
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AZ405411.1 GI:10529424
Other GSSs: OGVDL62TH
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 480)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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/clone lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOPO, Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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Fax: 301-438-0208
Email: whitelaw@tigr.org
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Brassica oleracea
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Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvattsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other CSSS: RPCI-24-26007.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Eax: 301 838 0200

Eax: 301 838 0200

Enail: szhaodetigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Ilbrary availability, please contact Pieter de Jong

(pdejong@mail.cho.org) Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm) BAC end

page: http://www.chori.org/bacpac/orderingframe.htm) BAC end

page: http://www.chori.org/bacpac/orderingframe.htm) Flate: 260 row: 0 column: 7

Seq primer: SP6

Class: BAC ends

Class: BAC ends

Seq primer: SP6

Class: BAC ends
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BZ042702
BZ042702.1 GI:23634332
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RPCI-24-26007.TJ RPCI-24 Mus musculus genomic clone RPCI-24-26007,
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/clone lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using Mool partially digested male C57BL/6J
DNA."
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                                                  81 AATCACACATTCATTAAGTAATATGAATGTAATTTA 118
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                        5 ACTIACACATICGTIAAGICATATATGTTTTGACTIA 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/60"
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/clone="RPCI-24-26007"
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BH051848.1 GI:14843837
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Acd28587 E. coli A	Acd28586 E. coli A	Acal5469 Prokaryot	Aas82555 DNA encod	Acd28591 E. coli A	Acd28590 E. coli A			Abli1816 Drosophil			Abl32626 Human imm	Abl21302 Drosophil	Abl34146 Human imm	Abl30408 Drosophil	Adc86000 Human GPC	Aad36260 Human G-p		Abg21634 Oligonucl	_	Abz32449 Candida a	Aac45407 Arabidops	Aac45408 Arabidops
SUMMARIES	ACD28587	ACD28586	ACA15469	AAS82555	ACD28591	ACD28590	ABN25854	ABL18112	ABL11816	ABL05790	ABL05792	ABL32626	ABL21302	ABL34146	ABL30408	ADC86000	AAD36260	ABV51050	ABQ21634	ABQ21635	ABZ32449	AAC45407	AAC45408
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Score	40	40	40	40	25	25	22.8	22.6	22	21.8	21.8	21.8	21.6	21.6	21.6	21.6	21.6	21.4	21.4	21.4	21.4	21.4	21.4
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## ALIGNMENTS

ArsR; arsenic resistance operon; biosensor; 88; arsenic. coli Arsk binding oligonucleotide CHROMLIB. ACD28587 standard; DNA; 40 BP 20-AUG-2001; 2001US-0313714P. 15-AUG-2002; 2002US-00222952. 10-OCT-2003 (first entry) (LAIN/) LAING L G. Bscherichia coli. US2003096275-A1. 22-MAY-2003. ACD28587; Laing LG; RESULT 1 ACD28587 

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the areanic resistance operan of E. coil) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid

sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds to a chromosomally expressed Arsk protein and is used in the biosensor of the invention

88888888

Sequence 40 BP; 17 A; 5 C; 7 G; 11 T; 0 U; 0 Other;

Gaps ö Length 40; 0; Indels Query Match
100.0%; Score 40; DB 8; I
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 40; Conservative 0; Mismatches 0;

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40 TAAGTCAAAAACAFATATGACTTAACGAATGTGTAAGTGC 40 1 TAAGTCAAAACATATATGACTTAACGAATGTGTAAGTGC

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E. coli Arsk binding oligonucleotide CHROML1T.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated noticel caid containing a specifically binds the analyte; (2) an isolated noticel caid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and an Arsk (encoded by part of the arsenic resistance operon of B. coli) protein comprising an anion acid sequence appearing as Aleb3440 binding to a nucleic acid sequence appearing as Aleb3440 binding to a nucleic acid sequence appearing a papearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligonucleotide which binds to a chromosomally expressed Arsk protein and is used in the biosensor of the 

BP; 11 A; 8 C; 5 G; 18 T; 0 U; 0 Other;

Length 42; Score 40; DB 8; I Pred. No. 4.9e-05; 100.0%; 100.0%; Query Match Best Local Similarity

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                    Zyskind JW;
Xu HH;
Gaps
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                                                                                                                                              Antisense; ss; prokaryotic essential gene; cell proliferation;
                                                                                                                              Prokaryotic essential gene antisense oligonucleotide #3339.
                                                                                                                                                                                                                                                                                                    Ohlsen KL,
Forsyth RA,
Indels
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Yamamoto R,
Mismatches
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                                                                                                                                                                                                                                                                                                      Malone C,
Carr GJ,
                                                                     ACA15469 standard; DNA; 401 BP
                                                                                                                                                                                                                                    21-MAR-2001; 2001US-00815242.

66-SEP-2001; 2001US-0094893.

25-OCT-2001; 2001US-0142923P.

98-FEB-2002; 2002US-0072851.

66-WAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107.
                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC
Conservative
                                                                                                                                                                                                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                              WPI; 2003-029926/02.
                                                                                                                                                                                      WO200277183-A2.
                                                                                                     27-OCT-2003
19-JUN-2003
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                                                                                                                                                       drug design
                                                                                                                                                                                                      03-OCT-2002
                                                                                      ACA15469;
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Wall D,
                                                                                                                                                                      Archaea.
Matches
                                                       RESULT 3
ACA15469
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the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a gene in an operon required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for rellular proliferation or the between compound that inhibits solidication of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the correction of an organism. The antisense nucleic acids required for cellular proliferation to isolate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational The invention relates to an isolated nucleic acid comprising any one of

required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the 6213 antisense sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 27-OCT-2003 to standardise OS field) Sequence 401 BP; 113 A; 68 C; 101 G; 119 T; 0 U; 0 Other; 88888888

.. 100.0%; Score 40; DB 7; Length 401; 100.0%; Pred. No. 5.7e-05; Ative 0; Mismatches 0; Indels Local Similarity 100. Query Match

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AASB2555 standard; cDNA; 2182 BP. RESULT 

AASB2555;

13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #18359.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

Homo sapiens

WO200175067-A2.

11-OCT-2001,

30-MAR-2001; 2001WO-US008631

31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167

(HYSE-) HYSEQ INC.

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73. P-PSDB; ABG18368.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 18359; 103pp; English.

The invention relates to isolated polynucleotide (1) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed sequence tags for identifying expressed contains the polynucleotides are also used in dissue, as molecular weight markers and as a food supplement. (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its bhinding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders in polypeptide and polynucleotide sequences have applications in displance in the produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and

amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences ន្តដូចមន្តន

Sequence 2182 BP; 516 A; 569 C; 582 G; 515 T; 0 U; 0 Other;

Gaps ö Query Match
100.0%; Score 40; DB 5; Length 21
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 40; Conservative 0; Mismatches 0; Indels è

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Length 2182;

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Gaps

ACD28591 standard; DNA; 25 BP

10-OCT-2003 (first entry)

B. coli Arsk binding oligonucleotide CHROMS1B.

ArsR; arsenic resistance operon; biosensor; ss; arsenic.

Escherichia coli.

US2003096275-A1.

22-MAY-2003.

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P.

(LAIN/) LAING L

Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated mucleic acid containing a specifically binds the analyte; (2) an isolated mucleic acid containing a containing a specific binding sequence that is bound specifically by the protein; and contained are a biosensor device for detecting the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and an Arsk (encoded by part of the arsenic resistance operon of B. coli) protein comprising an caid sequence that is at least 9% identical to anino acids 1-97 of the Arsk sequence appearing as ABUG3440 binding to a nucleic acid sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds to a chromosomally expressed Arsk protein and is used in the biosensor of the invention 

Sequence 25 BP; 13 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

62.5%; Score 25; DB B; Length 25; 100.0%; Pred. No. 11; Query Match Best Local Similarity us-10-676-299-6.rng

24-JUN-2002 (first entry)

ABN25854;

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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte, (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein of the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of the analyte in a sample, detecting the presence of an analyte in a sample, and are a control of the arsenic resistance operon of E. coil) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as ABU63440 binding to a nucleic acid sequence appearing oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligonucleotide which binds to a chromosomally expressed Arsk protein and is used in the biosensor of the
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Gaps
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding oligonucleotide CHROMS1T.
0; Mismatches
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                                                                                                                         1 TAAGTCAAAACATATATGACTTAA
                                                                      1 TAAGTCAAAACATATATGACTTAA
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                                                                                                                                                                                                                                                                                                                                ACD28590 standard; DNA; 25 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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ö Query Match 62.5%; Score 25; DB 8; Length 25; Best Local Similarity 100.0%; Pred, No. 11; Matches 25; Conservative 0; Mismatches 0; Indels

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ò 쉱 RESULT 7 ABN25854 ID ABN25854 standard; CDNA; 396

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; amineme deficiency; immune disorder; infectious disease; autoimmune disorder; hebumatoid arthritis; autoimmune thyroiditis; myasthenia gravis; gene; ss. Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders. Human ORFX polynucleotide sequence SEQ ID NO:20185 Disclosure; SEQ ID NO 20185; 1037pp; English. 30-MAY-2000; 2000US-0206132P. 29-AUG-2000; 2000US-0228716P. 29-MAY-2001; 2001WO-US010836 Shimkets RA, Leach MD; (CURA-) CURAGEN CORP. WPI; 2002-106308/14. P-PSDB; ABP10102. 40200192523-A2 Homo sapiens. 06-DEC-2001 

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ARNITS62 to ARNITS52 encode the human ORFX proteins given in ABPOUND to ABPIS00. ORFX proteins are useful for treating or preventing a pathology associated with a manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder: ORFX polymorleotide squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver. Described to a manufacture of a medicament for treating a sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver. Described to mineral disorders disorders related to organ transplantariton, cardiovascular diseases, disorders related to organ transplantariton, cardiovascular diseases, disorders related to organ transplantariton, cardiovascular diseases, disorders related to organ structure disorders such as multiple sclerosis, infectious diseases, autoimmune inflammatory eve disease. ORFX proteins are also disease and autoimmune inflammatory eve disease. ORFX proteins are also cueful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or leriodontal disease. And for gut protection or regeneration and treatment of lung or liver fibrosis, premic cycokine damage. NB. The sequence data for this patent did not systemic cycokine damage. NB. The sequence data for this patent did not formant disease and conditions resulting in each of the printed specification, but were observed to each of the printed specification, but were observed to each of the printed specification, in the sequence data for the printed specification, in the sequence of the printed specification in the sequence of the printed specification in the sequen form part of the printed specification, but was obtained in electronion format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Gaps ö DB 6; Length 396; Indels Sequence 396 BP; 148 A; 81 C; 51 G; 116 T; 0 U; 0 Other; Ċ 57.0%; Score 22.8; D 79.4%; Pred. No. 82; :ive 0; Mismatches Query Match
Best Local Similarity 79.43
Matches 27; Conservative

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3 AGTCAAAACATATATGACTTAACGAATGTGTAA 36

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272 AGTTAATAACATTTTTGTCTTTACAAATGTGTAA 305

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in bigher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1617-5 and the encoded proteins (ABB7737-Sequences (ABL16175) and the encoded proteins (ABB7737-ABB77072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                               Drosophila, developmental biology, cell signalling; insecticide, pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 5809.
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                                                                          ABL18112 standard; DNA; 6872 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                    23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 73.7.
Best Local Similarity 73.7.
Thos 28; Conservative
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            Drosophila melanogaster.
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                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABI16176-ABI30511), expressed DNA sequences (ABI16176-ABI30511), expressed DNA ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                             detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                                                                                                              Claim 1; SEQ ID NO 11852; 21pp + Sequence Listing; English.
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Myers BW;
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PWD,
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                                                           New isolated nucleic acid
genes from Drosophila and
interactions.
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Adams M,
                        WPI; 2001-656860/75
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Nes 26; Conserv
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                                      P-PSDB; ABB61687
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Venter JC,
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diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABILG176-ABILG1911), expressed DNA agequences (ABILG196-ABILG1911), expressed DNA ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format direct from WIPO at ftp.wipo.int/pub/published_pct_sequences
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ID ABL32626 standard; DNA; 19082
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                            Gaps
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pharmaceutical; gene; ds.
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                          Indels
    Pred. No. 2.5e+02;
0; Mismatches 7;
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Conservative
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, All'Ds, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                    Human; immune system disease; cytosine methylation; antiasthmatic; antiatriosclerotic; antianaemic; cytostatic; nootropic; antianaemic; antianaemic; cytostatic; nootropic; anticheumatic; anticonvulsant; ophthalmologica; antiinheumatic; antiarthritic; antidiabetic; antipsoriatic; antiminamatory; cancer; eye disease; arteriosclarosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal cytosine
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Human immune system associated gene SEQ ID NO: 2119.
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01-SEP-2000; 2000DE-01043826.
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23-MAR-2000; 2000US-0191637P, 11-JUL-2000; 2000US-00614150.

(PEKE ) PE CORP NY.

Venter JC, Adams M, Li PWD, Myers EW;

WPI; 2001-656860/75.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Claim 1; SEQ ID NO 42697; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1616-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 15933 BP; 4230 A; 3492 C; 3488 G; 4723 T; 0 U; 0 Other;

ö Gans .; 0 Query Match 54.0%; Score 21.6; DB 4; Length 15933; Best Local Similarity 75.0%; Pred. No. 2.9e+02; Matches 27; Conservative 0; Mismatches 9; Indels 0;

È 셤 Search completed: May 26, 2004, 17:50:07 Job time: 287.641 secs

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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	SULT 1  -09-601-198-111 Sequence 111, Application US/09601198 Betten No. 6531583 GENERAL INFORMATION: APPLICANT: Casell, Gail H. APPLICANT: Casell, Carryl R. APPLICANT: Lefkowitz, Bliot TITLE OF INVENTION: UREALFIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA FILE PRINTICATION NUMBER: US/09/601,198 CURRENT APPLICATION NUMBER: 60/073,189 PRIOR PLING DATE: 1998-01-30 PRIOR PLING DATE: 1998-01-30 PRIOR PLING DATE: 1998-01-30 SOFTWARE: PATENTIN VOT: 2.0 SEQ ID NO: 111 TYPE: DNA ORGANIEM: Ureaplasma urealyticum O9-601-198-111	Query Match  52.5%; Score 21; Best Local Similarity 82.8%; Pred. No. Matches 24; Conservative 0; Mismat. 2 AAGTCAAAAACATATATGACTTAACGAAT	SEGULT 2 Sequence 1066, Application US/09543681A Patent No. 6605709 GENERAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FILTE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709-1002-001 CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT APPLICATION NUMBER: US 60/128,706 PRIOR FILLING DATE: 1999-04-09 NUMBER: OF SEQ ID NOS: 8344
	199-11 191, 111, 111, 111, 111, 111, 111	atch cal Sim 24; 2 AA 46 AA	-681A-1 1066, 1066, 1006M INT: GA NT: GA NT: GA NT: GA NT: CA NT: CA NT: PILING NT: PILING
000000000000000044444 0000000000000000	RESULT 1 US-09-601-198-111 Sequence 111, Applic Patent No. 6531583 GENERAL INFORMATION: APPLICANT: Cassell, APPLICANT: Glass, APPLICANT: Lefkowi, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION IN PRIOR PULICATION NAMES OF SOLID NO. PRIOR PLING DATE: PRIOR PLING DATE: PRIOR PLING DATE: PRIOR PLING DATE: PRIOR APPLICATION NAMES OF SOLID NO. SOFTWARE: PALENTING DATE: PRIOR APPLICATION NAMES OF SOLID NO. SOFTWARE: PALENTING DATE: TYPE: DNA. SOFTWARE: PALENTING DATE: NUMBER OF SOLID NO. SOLID	uery Meest Loc atches	RESULT 2 US 09-543-681A-1066; Apple 1: Sequence 1066; Apple 2: Patent No. 660570; GENERAL INFORMATI APPLICANT: TITLE OF INVENTI TITLE OF INVENTI CURRENT FELLING DERICH PRICE APPLICATION PRIOR PAPLICATION PRIOR FILING DATE OF SEQ ID
0 00 0 000	MA D CONTRACTOR OF THE CONTRAC	දී කි	RESULT US-09-1 Paceul GENE APPI TITT FILL CURI PRIC

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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/607,384A

FILING DATE: 27-FEB-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BYRNEY THOMBER: 32,205

REGISTRATION NUMBER: 32,205

REGISTRATION NUMBER: 32,205

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 4:

ENDURING CHARACTERISTICS:

LENGIN 34 Deep pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid
                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: Streptococcus uberis , STRAIN: ATCC 27958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                             ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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            COUNTRY:
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                                                                                                                  Query Match 52.5%; Score 21; DB 4; Length 1275; Best Local SImilarity 73.0%; Pred. No. 51; Matches 27; Conservative 0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                         678 AGGTAAAAGAGATATAATTAAAGAAGGTGAAAGT 714
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Beffrey Gulcher:
TITLB OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09426290
Patent No. 6410712
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(128910)...(129139)
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; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1066
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US-09-426-290-1
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1636
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                                                         Gaps
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   DB 2; Length 342;
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51.0%; Score 20.4; DB 4; Length 825;
Best Local Similarity 71.1%; Pred. No. 81;
Matches 27; Conservative 0; Mismatches 11: Indela
                                                         Indels
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Query Match 51.0%; Score 20.4; D
Best Local Similarity 80.0%; Pred. No. 75;
Matches 24; Conservative 0; Mismatches
                                                                                                                S TCAAAAACATATGACTTAACGAATGTGT 34
                                                                                                                                                                       43 TCAAAACTAAATAAGACTTAACCAACGTGT 14
                                                                                                                                                                                                                                                                                                            Sequence 1636, Application US/09328352
Patent No. 6562958
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Patent No. 6489466
GENERAL INFORMATION:
APPLICANT: LADUNGA et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1636
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GENERAL INFORMATION:
APPLICANT: ALATOSSAVA, JOUKO TAPANI
APPLICANT: FORSMAN, P IVI TUULIKKI
APPLICANT: TILSALA-TIMISJ RVI, ANU KYLLIKKI
TITLE OF INVENTION: DNA SEQUENCE-BASED DIAGNOSIS OF MASTITIS
TITLE OF INVENTION: PROM A MILK SAMPLE

1100 NORTH GLEBE ROAD

ARLINGTON

STREET:

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V

US-08-607-384A-4/c; Sequence 4, Application US/08607384A; Patent No. 5849488

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APPLICANT: Charles Kunsch
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences NUMBER OF SEQUENCES: 5256
CORRESPONDENCES: 5256
CORRESPONDENCES: 5256
CORRESPONDENCES: 9410 Key West Avenue
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: Waryland
             Gaps
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REDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER BEADABLE FORM:

REDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-oct-1997

CLASSIFICATION NUMBER: 60/09,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INPORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46/789
           11; Indels
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                                                                                           1893 TATATCTAAAAATATATAACTTACTATATGTTTCAGT 1930
                                                     1 TAAGTCAAAACATATATGACTTAACGAATGTGTAAGT 38
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80.0%; Pred. No. 95;
tive 0; Mismatches 6;
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             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 443:
                                                                                                                                                                            US-08-956-171E-443/c
; Sequence 443, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5301 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 443:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Farina, Steven F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Conservative
           27; Conservative
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Best Local Similarity
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           Matches
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE REPERENCE: CLOOR842
CURRENT APPLICATION: WURBER: US/09/708,725A
CURRENT PELLING DATE: 2000-11-09
PRIOR FILLING DATE: 2000-11-09
PRIOR FILLING DATE: 2000-11-27
NUMBER: PSEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                    51.0%; Score 20.7;
71.1%; Pred. No. 88;
Pive 0; Mismatches 11; Indels
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B C000-09/620,312D
CURRENT PILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1473 AAAAAAAAAAATTGCCTTACACAATGTGTAAGTG 1510
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Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 572, Application US/09620312D
Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1).T.(2728)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-572
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NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL.FL_genes Version 1.0
SEQ ID NO 572
LENGTH: 2728
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 71.1
Matches 27; Conservative
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Zhang, Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang, Y. Tom
Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (202) .. (1212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                    ) LENGTH: 2199

) TYPE: DNA

) ORGANISM: Human

US-09-708-725A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-09-620-312D-572
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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PRIOR APPLICATION DATA:

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APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Mucleotide sequence of
The Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.0%; Score 20.4; DB 4; Length 1830121; 71.1%; Pred. No. 1.2e+02; tive 0; Mismatches 11; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             854524 TACGICAAAITGAAGTATGATTAAATGAATTTTTAAAT 854561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TAAGTCAAAACATATATGACTTAACGAATGTGTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFWARE: ASCII Text
CURRENT APPLICATION DATA:
PILING DATE: 23-ANG-2000
CLASSIFICATION: <University
                                                                       ATTORING DATE: UCN-5-1995
ATTORING PATE: UCN-5-1995
ATTORING AGENT INFORMATION:
NAME REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PB186P1C1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGRAT INPORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                    APPLICATION NUMBER: 08/476,102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.1<sup>1</sup>
Matches 27, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-643-990A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      용
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Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
TITLE OF INVENTION: The Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.0%; Score 20.4; DB 3; Length 35524; 71.1%; Pred. No. 1.1e+02; tive 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                         CADUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,137
FILING DATE: CLASSIFICATION AJ35
PRIOR APPLICATION AJ35
PRIOR APPLICATION NUMBER: US 60/024,700
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REFERENCE/DOCKET NUMBER: 31,215
REPRENCE/DOCKET NUMBER: 31,215
REPRENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20014 AAAACAAAAACACCTATGACTACATGAATGGGCGGGTG 20051
APPLICANT: Fisher, Krishna J.

TITLE OF INVENTION: Chimpanzee Adenovirus Vectors
NUMBER OF SEQUENCES:
5
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Chtr., P.O. Box (CITY: Spring House
STATE: Pennsylvania
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AAGTCAAAACATATATGACTTAACGAATGTGTAAGTG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

RAPPLICATION NUMBER:

RAPPLICATION NUMBER:

CLASSIPICATION: <a href="https://documents.com/">documents/</a>

CLASSIPICATION: <a href="https://documents.com/">documents/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 35524 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.1;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown;
MOLECULE TYPE: CDNA
US-08-923-137-1
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US-09-557-884-1
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ö g LENGTH: 1830121 base pairs

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Sequence 15, Application US/09499203
Facent No. 6570065
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KOSSMANN, Jens
APPLICANT: QUAXZ, Martin
APPLICANT: GUAXZ, Martin
APPLICANT: RUTH, Karola
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase
TILE REPERBNCE: 147-196F
CURRENT APPLICATION NUMBER: US/09/499, 203
CURRENT PILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                             Sequence 79, Application US/0886174E

Sequence 79, Application US/08861774E

Patent No. 6297007

GENERAL INFORMATION:

APPLICANT: Macers, Barbara

APPLICANT: Mac, Vivian

APPLICANT: Ho, Yap

APPLICANT: Ho, Yap

APPLICANT: Ho, Yap

TITLE OF INVENTION: BIOACTIVE MOLECULES

TITLE OF INVENTION: BIOACTIVE MOLECULES

TITLE OF INVENTION: BIOACTIVE MOLECULES

CURRENT FILING DATE: 1997-06-22

CURRENT FILING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 94

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 79

FIRM THE OF INVENTION OF SECOND NOS: PATENTIAL OF SECOND 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GTCAAAAACATATATGACTTAACGAATGTGTAAGTG 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB 3; ]
Pred. No. 1.1e+02;
0; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.2%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Usnea florida
US-08-861-774E-79
                                                                            RESULT 14
US-08-861-774E-79/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-499-203-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GARY BRETON
TITLE OF INVENTION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTBUS MIRABIL
TITLE OF INVENTION: NUCLEIC ACID AND THERAPBUTICS
FILE REFERENCE: 2709-1002-001
CURRENT PILLING DATE: 1090-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 3761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13

US-09-134-001C-1096/c

US-09-134-001C-1096/c

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GT-0.007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                         51.0%; Score 20.4; DB 4; Length 1830121; 71.1%; Pred. No. 1.2e+02; tive 0; Mismatches 11; Indels 0;
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Fred. No. 99;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                       854524 FACGTCAAAATGAAGTATGATTAAATGAATTTTAAAT 854561
                                                                                                                                                                                                                                                                                                                                                        1 TAAGTCAAAACATATATGACTTAACGAATGTGTAAGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 TCAAAAACATATATGACTTAACGAATGTGTAAGTGC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 TAAGATAAAAATAATGCCTTATTAAATGTG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TAAGTCAAAACATATATGACTTAACGAATGTG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.2; D
Pred. No. 87;
0; Mismatches
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-543-681A-3761/c
; Sequence 3761, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA; CRANISM: Staphylococcus epidermidis US-09-134-001C-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.5%;
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Best Local Similarity 72.2%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Proteus mirabilis
US-09-543-681A-3761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.8
Matches 25; Conservative
                                                                                                                                                                                                                                             Best Local Similarity 71.1
Matches 27; Conservative
                                                                                                                                              US-09-643-990A-1
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May 26, 2004, 16:21:09; Search time 2771.45 Seconds (without alignments) 430.997 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                         55026578
                                                                                                                                                                                                               1 taagtcaaaaacatatatgacttaacgaatgtgtaagtgc 40
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                   27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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60.5 880 28 BZ38B776 60.0 502 12 BMS39131 59.0 255 29 CG231937 59.0 420 28 AZ405411 59.0 480 29 CG197578 59.0 649 28 BH051848 59.0 905 28 CC400118 59.0 905 29 CG182590 59.0 1020 29 CG182586 58.5 1064 28 BH744046 57.5 375 28 AQ137091 57.5 861 29 EX73966	CG052813 CG052813 CG052813 CG052815 BB032011 BB032011 BB032011 BB032045 BZ751549 BZ751554 BZ7	56.5 699 29 CCG56781 CCB5678 56.5 700 29 CER22849 CCB56781 CCB5678 56.5 762 29 CER028178 CER02817 56.5 764 29 CGG53250 CGG012525 56.5 804 29 CGG13250 CGG13255 56.5 804 29 CGG13832 EH520708 EH520708 56.5 813 28 EH52058 EH54258 EH54255 56.5 8148 29 CGG175594 CGG17359 56.5 861 29 CGG17594 CGG17359 56.5 882 29 CC690601 CC690601	BM307747  sak33d01.y1 Gm-c1075 Glycine max cDNA clone SOYBEAN CLONE ID: 6m-c1075-4777 5', mRNA Bequence. BM307747  BM307747.1 GI:18039453  BSY. Glycine max (soybean)	GlyCine.  (1) (bases 1 to 233)  Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Shomna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCarn, R., Waterston, R. and Wilson, R. Public Soybean EST Project Unpublished (1999) Contact: Shoemaker R/Public Soybean EST Project Contact: Shoemaker R/Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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BM307747 AW458707 BM568294 BE824180

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233 481 525 640

62.0 62.0 62.0

24.8 24.8 24.8

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Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800) 553-4563 or contact via email: ccu@resgen.com
Insert Length: 1046 Std Error: 0.00
Seq primer: -40RP from Gibco
Seq primer: -40RP from Gibco
High quality sequence stop: 411.
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1 (bases I to 525)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Banna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Mylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCan, R., Materston, R. and Wilson, R.

Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.0%; Score 24.8; DB 10;
ilarity 80.6%; Pred. No. 2e+02;
Conservative 0; Mismatches 7;
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//done liber@m-cl075"
//done liber@m-cl075"
//done liber@m-cl075"
//done liber@m-cl075"
//done liber@m-cl075"
//done liber@m-cl078 liber.
//done differentiating somatic embryos cultered on MSM6AC.
The library was prepared using the Stratagene pBluescript
II SK(+) library construction Xit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an XhoI restriction site. EcoRI
adaptors were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
followed by XhoI digestion. The cDNA fragments
followed by Storiction site of the pBluescript vector. The ligated cDNA fragments
were transformed into the Booll-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into z.coli slettroMax DH10B host cells.
Tissue culture and library construction were performed by
Francoise Thibaud-Nissen and Anu Khana (Lila Vodkin lab,
           Tel: 314 286 1800

Rax: 314 286 1800

Exa: 314 286 1810

Exail: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccu@resgen.com web site:

www.resgen.com

seq primer: -40RP from Gibco

High quality sequence stop: 223.

High quality sequence stop: 223.
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Shoemaker,R., Kežm,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Fylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBBAN CLONE ID: Gm-c1075-4777"
/fissue_type="differentiating somatic embryos cultered on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TAAGTCAAAACATATATGACTTAACGAATGTGTAA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Illinois)."
                                                                                                                                                                                                                                                                                                                       organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lab_host="DH10B"
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Best Local Similarity 80.6
Matches 29; Conservative
                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
/clone lib="dem-clo57"
/clone lib="dem-clo57"
/note="Vector: paluescript II SK+; Site 1: EcoR1; Site 2:
/note="Vector: paluescript II SK+; Site 1: EcoR1; Site 2:
Xho1; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 2 week old seedlings from
P1468916. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dr) sequence with a
Xho1 restriction site. EcoR1 adapters were ligated to the
blunt-ended cDNA fragments followed by Xho1 digestion.
The cDNA fragments were directionally cloned into the
EcoR1-Xho1 restriction site of the paluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEB24180 640 bp mRNA linear BST 24-MAY-2001
GM7100023A20B3 Gm-r1070 Glycine max cDNA clone Gm-r1070-8886 3',
mRNA sequence.
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Other ESTS: AWS6832 corresponding to Gm-r1030-3256 (5')
Contact: Vodkin, L.O., Pl. A. Functional Genomics Program for Soybean (NSF 9872565)
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Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Fabaceae; Papilionoideae; Phaseoleae;
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Fax: (217) 233-4582
Email: 1-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (808) 519-3324 or (314)
427-3324 or contact:clonesystems.com or info@genome
ystems.com web site:www.genomesystems.com
Seg primer: 5'-TETTTTTTTTTTTTT(A/C/G)-3'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                  /organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1057-4063"
/tissue_type="Degenerating cotyledons, 2 week old seedling"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.0%; Score 24.8; DB 12; Length 525; 80.6%; Pred. No. 2e+02; 7; Indels 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 TAAGTCGAAAATATATGATTTAGCGAATGAATTA 423
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BE824180.1 GI:10256414
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Glycine max
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1 (bases 1 to 640)
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Best Local Similarity
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COMMENT
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Bukaryota; Bntamoebidae; Entamoeba.

Bukaryota; Bntamoebidae; Entamoeba.

Wang, Z., Samuelson, J., Clark, C.G., Eichinger, D., Paul, J., van Dellen, K., Hall, M., Anderson, T. and Loftus, B.

Den discovery in the Entamoeba invadens genome

Mol. Biochem. Paraeitol. 129 (1), 23-31 (2003)
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80.6%; Pred. No. 2e+02;
Live 0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TAAGTCAAAACATATATGACTTAACGAATGTGTAA 36
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DNA was provided by Daniel Eichinger
SNA primer: TF
Class: sheared ends.
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Contact: Brendan Loftus
Department of Bukaryotic Genomics
organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Query Match

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QCVDIGZYV ZM 0.7_1.5_XB Zea mays genomic clone ZMMBMa0511K04, genomic survey sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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1M0174A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M017AA13 F, genomic survey sequence.
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/clone lib="Zm, 0.7 1.5 KB"
/clone lib="Zm, 0.7 1.5 KB"
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center Drive, Rockville, MD 20850, USA
                                              Indels
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Best Local Similarity 75.0%; Pred. No. 3.8e+02; Matches 30; Conservative 0; Mismatches 10;
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
Other GSSs: OGVDL62TH
Contact: Cathy Whitelaw
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Class: sheared ends.
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Tel: 301-838-5843
Fax: 301-838-0208
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Zea mays
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                                                                      /mol type="genomic DNA"
/#nol type="logic DNA"
/#nol type="genomic DNA"
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/clone="lip="caniss CDNAs from testes cells"
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/clone="taxo
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Expressed sequence tags from Canis familiaris (dog) (2002) Unpublished (2002)
Contact: W. Richard McCombie
Lite Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Carnivora, Pissipedia, Canidae, Canis.

[ (bases 1 to 502)
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    1, .88U
/organism="Entamoeba invadens"
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Plate: hb05 row: c column: 02
Seq primer: -21Ml3UnivRev
High quality sequence stop: 502.
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Canis familiaris
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

TITLE JOURNAE COMMENT

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GSS 03-OCT-2000

Query Match

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    .649
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host-"B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="mouse 10kb plasmid UUGCIM library"
/note="Westor: PWD42Dry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Genome Center
Was 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 480)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0174 row: A column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/6J"
                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 420. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:10090"
/clone="UUGC1M0174A13"
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                                                                        Unpublished (2000)
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AUTHORS
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ACCESSION

RESULT 9

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ORIGIN

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Tagagaye, G. Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.

Russell, D., de Jong, P. and Fraser, C.M.

Moublished (1999)

Other_GSS: RPCI-24-26007.TV

Contact: Shaying Zhao

Other_GSS: RPCI-24-26007.TV

Contact: Shaying Zhao

Department of Rukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Email: Salva@efigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Clones are derived from the mouse BAC library RPCI-24. For BAC

Clones are derived from the mouse BAC library RPCI-24. For BAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC

Resources (http://www.chori.org/bacpac/orderingframe.htm).

Plate: 260 row, 0 column: 7

Seq prime: Sp6

Class: BAC ends
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RPCI-24-26007.TJ RPCI-24 Mus musculus genomic clone RPCI-24-26007,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4577"
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COT selected genomic DNA library"
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Sukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 649)
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                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850, USA
Par: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 TABATTACATTCATATATTACTTAATGAATGTGTGATT 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Zea mays"
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFMC4TB
Contact: Cathy Whitelaw
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CC400118 905 bp DNA linear GSS 19-MAY-2003 PUHPP62TB ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa505K04, genomic survey sequence.
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Bukaryots, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae;

1 (bases 1 to 904)

Whitelaw.C.A., Quackenbush,J., Van Aken,S., Utterback,T.,

Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and

Maize Genomics Consortium

Unpublished (2003)
                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Tracheophyta, Spermatophyta; Magnoliophyta; Liliopsida; Poales, Poaceae, PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 905)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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/mol type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa505K04"
/clone="ZMMBTa505K04"
/note="Weetor: pCR4-T0F0; Sire 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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P12 Medical Center Drive, Rockville, MD 20850, USA
P13 301-838-8843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 TAAATTACATTCATATTACTTAATGAATGTGTGATT 302
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Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUHPP62TD
Contact: Cathy Whitelaw
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CG182590
CG182590.1 GI:34073651
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CC400118,1 GI:30880208
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Bukaryophyta, Puridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacea, Brassica.

E (bases 1 to 703)

B Delehaurey, K., Pewell, G., Pulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, K.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: 1jq76 row: c column: 05
Seq primer: -21UPpOT forward
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: snocgune feart: 94
High quality sequence stop: 551.
High quality sequence stop: 551.
Location/Qualifiers
1. 0.03
| organism="Brassica oleracea" | fmo. 170a | fgenomic DNA" | fmo. 170a | fgenomic DNA" | fmo. 150a | f
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                                                               /cione_ips_mprecu/stain"
/rote="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
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                                                                                                                                                                                                                                                                                                                                                            59.0%; Score 23.6; DB 28; Length 649; larity 76.3%; Pred. No. 5e+02; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.0%; Score 23.6; DB 28; Length 703; 76.3%; Pred. No. 5e+02; live 0; Mismatches 9; Indels 0;
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'clone="RPCI-24-26007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ042702
BZ042702.1 GI:23634332
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Best Local Similarity
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Best Local Similarity
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 11 BZ042702

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ORIGIN

ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

source

FEATURES

RESULT 12 CC400118/c

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Gaps

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Query Match
                                                                                                                                ACCESSION
VERSION
KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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| Organism="Zea mays" | Organism="Zea mays" | Organism="B73" | Organism="B73" | Organism="Zea" | O
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Zea mays
Makaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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/clone_lib="zm 0.6_1.0 KB"
/note="Vector: pCR4_TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 59.0%; Score 23.6; DB 29; Length 969; 1 Similarity 76.3%; Pred. No. 4.9e+02; 29; Conservative 0; Mismatches 9; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5643 Fax: 301-838-6030 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TAAGTCAAAAACATATATGACTTAACGAATGTGTAAGT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA" /strain="B73"
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Class: sheared ends.
   Location/Qualifiers
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1. .1020
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Unpublished (2003)
Other GSSs: PUKCN17TD
Contact: Cathy Whitelaw
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CG182586.1 GI:34073647
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Class: sheared ends.
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Best Local Similarity
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Best Local Similarity
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SOURCE
ORGANISM
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DEFINITION
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VERSION
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JOURNAL
COMMENT
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CG182586
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AUTHORS
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                                                              PEATURES
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RESULT 15

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1064 bp DNA linear GSS 09-OCT-2001
T005 RFLP clone from soybean genomic DNA Glycine max genomic clone
PH174046
                                      GSS 09-OCT-2001
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="RFLP clone from soybean genomic DNA" force="Vector: pBS+; PSI-generated fragments of genomic DNA. Library construction described by Keim, P. & Shoemaker, R.C. (1988) Soybean Gen. News. 15:147-148."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agronomy Department USDA-ARS and Iowa State University USDA-ARS and Iowa State University G304 Agronomy Hall, Ames, IA 50011-1010, USA Tel: 515 294 1205.
Fax: 515 294 2299.
Email: dgrantediastate.edu single pass sequence class: RFLP clone.
                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1064)
Grant, D. and Shoemaker, R.C.
unpublished sequence of soybean RFLP probe
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AGTCAAAAACATATATGACTTAAGGAATGTGTA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Glycine max"
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1. .1064
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Job time : 2773.45 Becs
                                                                                                                                           BH174046.1 GI:15989413
                                                                                                                                                                                                    Glycine max (soybean)
Glycine max
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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Ruminantia; Pecora; Bovoidea;
Bovidea; Bovinae; Bos.

1 (Dases 1 to 774)

23 Lin,S., Majar,R.Z., Adelson,D., Gill,C.A. and Roe,B.A.

Bovine BAC End Sequences from Library TAMBT
Upublished (2001)

41 Contact: Bruce A. Roe
Advanced Center for Genome Technology
University of Oklahoma Department of Chemistry and Biochemistry
620 Parrington Oval, Room 208, Norman, OK 73019, USA
Tel: 405 325 7762
Email: broe@ou.edu
Class: BAC ends
High quality sequence start: 39
High quality sequence stop: 668.
AQ788301 HS 3143_A
CC814073 ZWWHBCO51
CC419273 PUHGBG051
CC419273 PUHGBG075
AL097067 Drosophil
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BM171079 EST57602
BZ8252499 PUFEQ31TB
BM171079 EST57602
BZ825249 PUFEQ31TB
BM171079 EST573602
BZ8252499 PUFEQ31TB
BB373536 BB373536
BB420422 BB420422
BF449847 maad2bb6.
AA575651 AN56b03.r
                                                                                                                                                                                                                                                                                                                                                                                                                                       1774 bp DNA linear GSS 08-AUG-2003 tO78e02ba.fl TAMBT Bos taurus genomic clone t078e02ba, genomic CC924563
                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                           AV382514
BK857902
AQ016199
BG307569
BM184130
BM095920
BM183874
 AQ788301
CC819273
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CC80020H
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BX111664
BX1166363
AQ035362
BX1166363
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BM171079
BZ822499
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BM226209
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AZ897507
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                                                                                                                                                                                                                                                                         BI926826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC924663.1 GI:33560002
GSS.
 Bos taurus (cow)
Bos taurus
                  RESULT 1
CC924663
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
CC924663 t078e02ba
BX134638 Danio rer
AZ753174 RPCI-24-8
CG009365 ZUAET89TV
                                                           May 26, 2004, 16:21:09; Search time 1593.59 Seconds (without alignments) 430.997 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                  27513289 segs, 14931090276 residues
                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                 US-10-676-299-7
23
1 ttaatcatatgogtttttggtta 23
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_esthum:*
em_estin:*
em_estov:*
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gb_est1:*
gb_est2:*
gb_htc:*
gb_est2:*
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82.6
81.7
81.7
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19.4 19.4 18.8

Score

No. Result

PEATURES

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/strain="C57BL/6J"
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/clone="RPCI-24-82118"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 TIAATCATAAGGGTTTTTGGTT 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 82 row: 1
Seq primer: T7
Class: BAC ends.
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Zea mays
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CG009365/c
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Actinopterygii, Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 775)
S Humphray, S.U., Huckle, E. and Durham, J.L.
Direct Submission
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
humquery@sanger.ac.uk Unpublished from the SP6 end of BAC 91C22. 91C22 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rexio/.
                                                                                                              /Gex="wale" (cell type="Blood" (cell type="Blood" (cell type="Blood" (cell type="Blood" (cell type="Vector: pBeloBaCil; Site_1: Hindill; Site_2: Hindill; TAMBT Bovine BAC library (Wale) produced by Texas A&M University, Department of Animal Science."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616 bp DNA linear GSS 25-JAN-2001

FPCI-24-82118.TV RPCI-24 Mus musculus genomic clone RPCI-24-82118,

A2753174

A2753174.1 GI:12538333

GSS.
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                                              /mol_type="genomic DNA"
/strain="Angus bull T A M U Shoshone Y6 11519666"
/db_xref="taxon:9913"
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Best Local Similarity 95.2%; Pred. No. 4.5e+02;
Matches 20; Conservative 0; Mismatches 1;
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100.0%; Pred. No. 6.6e+02;
iive 0; Mismatches 0;
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/db_xref="taxon:7955"
/clone="DrEY-91C2"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
                               'organism="Bos taurus"
Location/Qualifiers
                                                                                                     'clone="t078e02ba"
                                                                                                                                                                                                                                                                                                                                                                    658 raarcararccarrarccar 678
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BX134638.1 GI:27965929
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Danio rerio
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Best Local Similarity 100.
Matches 19; Conservative
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AZ753174/c
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AUTHORS
TITLE
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BX134638
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FEATURES

ORIGIN

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COMMENT

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5003 Sequence. 694 bp DNA linear GSS 19-AUG-2003 ZUAET89TV ZM 3.0 4.0 KB Zea mays genomic clone ZAMBPa0045010, GENOMIC SULVEY SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Spleen/Brain"
/cell_type="Spleen/Brain"
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/note="Wector: prARRAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Wouse BAC Library produced by Pieter Ge Jong. The library was cloned in the prARBAC1 cloning vector at the BamH1 sites using MboI partially digested male CS7BL/6J DNA."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Cliek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSS: ZUAETRSTH
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ZMMBBC0518K14f ZMMBBc Zea mays subsp. mays genomic clone
ZMBBC0518K14 5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                 Zea mays subsp. mays
Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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/db_xref="taxon:4578"
/clone="xxwbacc518X14"
/lab_host="E. coli DH108"
/clone lib="xxwbac"
/note="Vector: pTARBAC1.3; Site_1: BamH1; Site_2: BamH1"
                                                                                  Gaps
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Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003b)
Unpublished (2003)
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                                              Length 752;
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Tel: 732 445 3801
Fax: 732 445 5735
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Pred. No. 8e+02;
0; Mismatches 2;
                                          81.7%; Score 18.8; DB 28; 90.9%; Pred. No. 8.1e+02; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: T7
Class: BAC ends
High quality sequence start: 71.
Location/Qualifiers
                                                                                                                                                               306 rraarcaahtecerrirreerr 327
                                                                                                                      1 TTAATCATATGCGTTTTTGGTT 22
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90.9%;
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CC419273
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ788301 GSS 03-AUG-1999
HS_3143_Al_G12_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3143 Col=23 Row=M, genomic survey
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                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone="zxwBPa0045010"
/clone lib="zxl 3.0 4.0 kB"
/note="Vector: BBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-368
Fax: (206) 616-3897
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3143 row: M column: 23
Seq primer: Mi3 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   Length 694;
TIGR Medical Center Drive, Rockville, MD 20850, USA 9712 Medical Center Drive, Rockville, MD 20850, USA FER: 301-838-543 Pax: 301-838-0208 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                   ch 81.7%; Score 18.8; DB 29;
1 Similarity 90.9%; Pred. No. 8.1e+02;
20; Conservative 0; Mismatches 2;
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/ Organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=3143 Col=23 Row=M"
                                                                                                                                                                             /organism="Zea mays"
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/strain="B73"
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Location/Qualifiers
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                                                                                                   Seq primer: TF
Class: sheared ends
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/organism="Medicago truncatula"
/mol type="genomic DNA"
/mol type="genotype A17"
/dolf="taxen:3880"
/clone="low16-030"
/clone="low16-030"
/clone lib="shotgun sub-library of BAC clone low16"
/clone lib="shotgun sub-library of BAC clone low16"
/clone sheared BAC DNA subcloned into the Smal site of puclos the template DNA for sequencing was obtained by PCR using universal primers is Sequencing reactions were primed from the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA)
in the pUC18 polylinker."
                                                                                                                                                                                                                                                                                                                                                                                  AZ045495 14-MAR-2000 DNA linear GSS 14-MAR-2000 T234126b shotgun sub-library of BAC clone 10M16 Medicago truncatula AZ045495
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T234299b shotgun sub-library of BAC clone 12G15 Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dcookappserver.tamu.edu
Other name: BSC-2D-030; date: 3/1/00; Submitted to the Database of
Genome Survey Sequences (GSS) on 03/13/00; More information is
available at http://chrysie.tamu.edu/medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 354)
Xish, L. Baek, J., Lim, H., Peng, H., Bllis, L. and Cook, D.R.
BAC survey sequencing of Medicago truncatula (2000a)
Unpublished (2000)
                                                                                                            Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cook DR.
The Crop Biotechnology Center
Trexas A&M University We are the Crop Electron State of Plant Pathology and Microbiology, RM Peterson Bidg, College Station, TX 77843-2132, USA Pax: 409 862 4790
                                                                                                                                                              Indels
                                                                                                            29;
                                                                                                            Score 18.8; DB 2
Pred. No. 8e+02;
0; Mismatches
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             /plasmid="pBeloBAC11"
/note="end : T7"
                                                                                                                                                                                                                                             278 TAAATCATATGCGTTT 299
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                                                                                                            Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative
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Class: BAC subclone.
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Matches 19; Conserv
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Submitted (23-UTL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr.)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1. (bases 1 to 973)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bernetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="ZMBTa414P05"
/clone="Ib-"ZM 0.6.1.0 XB"
/note="Weetor: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN01003 of DrosBAC library from Drosophila melanogaster (fruit
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.7%; Score 18.8; DB 28; Length 973; larity 90.9%; Pred. No. 8e+02; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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/clone="BACN01003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Zea mays"
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                                                                                                                                                      Maize Genomics Consortium
                                                                                                                                                                                                                                                                                                                               Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                           Unpublished (2003)
Other GSSs: PUHBQ87TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL097067.1 GI:5608678
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Class: sheared ends
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/clone lib-shotgun sub-library sequences were obtained
from sheared BAC DNA subcloned into the Smal site of
pUG18. The template DNA for sequencing was obtained by PCR
using universal primers. Sequencing reactions were primed
from the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA)
in the pUG18 polylinker."
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                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: dcook@ppserver.tamu.edu
Other name: BSC-3D-011; date: 3/1/00; Submitted to the Database of
Genome Survey Sequences (GSS) on 03/13/00; More information is
available at http://chrysie.tamu.edu/medicago.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Department of Plant Pathology and Microbiology, Rm 120 L.F.
Beterson Bldg, College Station, TX 77843-2132, USA
Tel: 409 845 84790
                                                                                                                                                                                                       1 (Sases 1 to 475)

Kim, D., Baek, J., Lim, H., Peng, H., Ellis, L. and Cook, D.R. BAC Survey sequencing of Medicago truncatula (2000a) Unpublished (2000)

Contact: Cook DR

The Crop Biotechnology Center
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Kim,D., Back,J., Lim,H., Peng,H., Bllis,L. and Cook,D.R.
BAC survey sequencing of Medicago truncatula (2000a)
Unpublished (2000)
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genomic clone 12G15-011, genomic survey sequence.
AZ045618
AZ045618.1 GI:7240056
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/organism="Medicago truncatula"
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                                                                                    Medicago truncatula (barrel medic)
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The Crop Biotechnology Center
Texas A&M University
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Class: BAC subclone
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/mol type="genoided DNA"
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Department of Plant Pathology and Microbiology, Rm 120 L.F. Peterson Bldg, College Station, TX 77843-2132, USA Tal: 409 845 8743
Fax: 409 862 4730
Email: dccock@ppserver.tamu.edu
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Cockeppserver.tamu.edu
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Cockeppserver.tamu.edu.modu.modited to the Database of
Cockeppserver.tamu.edu/modicago.
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Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabates; Pabaceae; Papilionoideae; Trifolieae;
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Department of Plant Pathology and Microbiology, Rm 120 L.F.
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Deterson Bldg, College Station, TX 77843-2132, USA
Tel: 409 845 8713
Pax: 409 862 4790
Pax: 409 862 4790
Cher name: BSC-2-08; date: 3/3/99; Submitted to the Database of Genome Survey Sequences (GSS) on 06/01/99; More information is available at 'http://chrysie.tamu.edu/medicago',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Kim, D., Peng, H., Ellis, L. and Cook, D.R.
BAC survey sequencing of Medicago truncatula
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cook DR
The Crop Biotechnology Center
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Class: BAC subclone.
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Class: BAC subclone.
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Best Local Similarity
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/ organism="trasmonium yoeill yoeill"
/ nol type="mRNA"
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/ clone lib="pyBS"
/ lab bost="E. coli XL-1 Blue"
/ clone lib="pyBS"
/ lab bost="E. coli XL-1 Blue"
/ parasites, and leukocytes removed by passage over
microcrystalline cellidose collumns. Total RNA was
record strand supparated on the presence of
size-fractionated clone with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with Xnol and separated on a Sephacryl S-500 column.
Size-fractionated clone was pagent was cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                              Plasmodium yoelii yoelii

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Loases 1 to 309)

Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,

Fraser,C.M. and Carucci,D.J.

Plasmodium yoelii EST project at TIGR

Unpublished (2001)

Contact: Jane Carlton

Paraite Genomics Group

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-530-9319

Fax: 301-838-0208

Email: carlton@tigr.org

For clone info, please contact the Malaria Research and Reference

Reagent Resource Center, ATCC

Reagent Resource Center Reagent Reagent
                                                                                                        BM164586
EST567109 PyBS Plasmodium yoelii yoelii cDNA clone PYCLW28 5' end,
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                                                                                                                                                                                                                         BM164586
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                                  RESULT 14
BM164586
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/organism="Medicago truncatula"

/organism="genocype A17"

/ob xref="taxon:380"

/clone="lb="shotgun sub-library of BAC clone 10M16"

/clone="lb="shotgun sub-library of BAC clone 10M16"

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in the pUC18 polylinker."
/clone_lib="shotgun sub-library of BAC clone lowi6" hote="Vector: pUCIB: BAC survey sequences were obtained from sheared BAC DNA subcloned into the Smal site of pUCIB. The template DNA for sequencing was obtained by PCR using universal primers. Sequencing reactions were primed from the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA) in the pUCIB polylinker."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cook Man University The Crop Biotechnology Center Theas akm University Department of Plant Pathology and Microbiology, Rm 120 L.F. Department of Plant Pathology and Microbiology, Rm 120 L.F. Peterson Bldg, College Station, TX 77843-2132, USA Fex: 409 845 8473

Email: dcook@ppserver tamu.edu
Chern name: BCC-2.37; date: 3/3/99; Submitted to the Database of Genome Survey Sequences (GSS) on 06/01/99; More information is available at 'http://chrysie.tamu.edu/medicago'.
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1 (bases 1 to 655)
Kim,D., Peng,H., Ellis,£. and Cook,D.R.
BAC survey sequencing of Medicago truncatula
Unpublished (1999)
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Medicago truncatula
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143 bp mRNA linear EST 18-JUN-1999 LTSB911.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219684 3', AI738836
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Length 309;
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Query Match 79.1%; Score 18.2; DB 12; Best Local Similarity 87.0%; Pred. No. 1.4e+03; Matches 20; Conservative 0; Mismatches 3;
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Query Match 79.1%; Score 18.2; DB 9; Length 343; Best Local Similarity 87.0%; Pred. No. 1.4e+03; Matches 20; Conservative 0; Mismatches 3; Indels (

1 TEAATCATATGCGTTTTTGGTTA 23

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May 26, 2004, 15:22:28 ; Search time 178.526 Seconds (without alignments) S94.900 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			d			SUMMARIES				
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Ų	16	38.6	74.4	668	ເດ	ABA19908	Ž	Aba19908 B	Human	n nez
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ABA18949	ABA19906	ABA18948	ABA20196	ABL33591	ABL92277	AAD22328	AAK84424	AAK84423	ABL34124	ABL92318	ABL32465	AAS33559	AAS34560	AAZ97081	ACH66710	AAL43413	ABL49301	AAL03182	ACP30939	ACP30938	ADC86642	
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## ALIGNMENTS

ArsR; arsenic resistance operon; biosensor; ss; arsenic. E. coli Arsk binding oligonucleotide CHROMSIB. BP. 20-AUG-2001; 2001US-0313714P. 15-AUG-2002; 2002US-00222952. RESULT 1 ACD28591/c ID ACD28591 standard; DNA; 25 (first entry) Escherichia coli. US2003096275-A1. 10-OCT-2003 22-MAY-2003. ACD28591; 

(LAIN/) LAING L G. Laing LG;

WPI; 2003-576876/54.

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of a analyte in a sample, detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the arsenic resistance operno of E. coli) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid

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Gapa

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Indels

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Mismatches

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Conservative

25;

Matches

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Gaps

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sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds to a chromosomally expressed ArsR protein and is used in the biosensor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  presence of analyte in a sample comprising: (1) an isolated protein that specifically binding the analyte; (2) an isolated mucleic acid containing a specifically binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein; and biosensor device for detecting the presence of an analyte, Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and an are comprising an anno acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABU63440 binding to a nucleic acid sequence appearing as ABU63440 binding to a nucleic acid system is useful for detecting the presence of analyte in a sample. The presence comprising oligomicleotides appearing as ABU63460 binding to a nucleic acid system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligomicleotide which binds to a chromosomally expressed ArsR protein and is used in the biosensor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a new system (biosensor) for detecting the
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                                                                                                                                                                   Score 25; DB 8; Length 25;
Pred. No. 1.6;
                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArsR; arsenic resistance operon; biosensor; ss; arsenic.
                                                                                                                              Sequence 25 BP; 13 A; 3 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 7 A; 2 C; 3 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli Arsk binding oligonucleotide CHROMS1T.
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                1 TRAGICATAIATGTITITGACTIA 25
                                                                                                                                                                                                                                                                     100.0%; Scu-
100.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 35; Page 15; 36pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-2002; 2002US-00222952
                                                                                                                                                                                                                                                                                                                                                                                   ACD28590 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-576876/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyte in a sample.
                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003096275-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                          ACD28590;
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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein; or the mucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, and an Arsk (encoded by detecting the presence of an analyte in a sample, and one of a sequence that is at least 90% identical to amino acids 1-97 of the Arsk sequence appearing as ABG540 binding to a nucleic acid the Arsk sequence appearing as ABG540 binding to a nucleic acid sequence comprising ollgomucleotides appearing as ABG5864-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligomucleotide which binds to a chromosomally expressed Arsk protein and is used in the biosensor of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system comprising isolated protein and nucleic acid, and a detection sem that indicates a change in binding of the protein to the nucleic in the presence of the analyte, useful for detecting the presence of
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                                                                                                                                                                                                                                                                               ArsR; arsenic resistance operon; biosensor; ss; arsenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40 BP; 17 A; 5 C; 7 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                           B. coli Arsk binding oligonucleotide CHROML1B.
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                                                                                                                            ACD28587 standard, DNA; 40
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Matches 25; Conser
                                                                                                                                                                                                                                                                                                                     Escherichia coli
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                                                                                                                                                                  ACD28587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laing LG;
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ACD28586 standard; DNA; 42

ACD28586 ID ACD2

Score 25; DB 8; Length 25; Pred. No. 1.6;

100.0%;

Query Match Best Local Similarity

21-MAR-2002; 2002WO-US009107

WO200277183-A2 03-0CT-2002

Archaea.

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The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein: or the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, at the area of the order order of the order of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of
                                                                                                                                                                                                                        ArsR; arsenic resistance operon; biosensor; ss; arsenic
                                                                                                                                                      E. coli ArsR binding oligonucleotide CHROMLIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 35; Page 15; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2002; 2002US-00222952.
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                                                                                          10-OCT-2003 (first entry)
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                                                                                                                                                                                                                                                                                    Escherichia coli.
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                                 ACD28586;
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Gaps ö 100.0%; Score 25; DB 8; Length 42; 100.0%; Pred. No. 1.6; 0; Indels Sequence 42 BP; 11 A; 8 C; 5 G; 18 T; 0 U; 0 Other; 100.0%; Prec. ... Local Similarity 100. ses 25; Conservative Query Match Best Loc. Matches

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BP

Prokaryotic essential gene antisense oligonucleotide #3339.

Antisense; ss; prokaryotic essential gene; cell proliferation;

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The invention relates to an isolated mucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid condaining the vector; (3) an isolated condaining the vector; (3) an isolated polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding collypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that that inhibits cellular proliferation, (6) identifying a gene required for cellular proliferation or the biological pathway required for proliferation, or that thinbits cellular proliferation of an organism acts; (9) manufacturing an antibicit; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibicit; (10) profiling a compound that inhibits or organism acts; (9) manufacturing an antibicit; (10) profiling a compound that inhibits the product is oversypressed or undersepressed; (12) determining the extent or to which each of the strains is present in a culture or collection of strains; or (13) identifying proteins or screening for homologous nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids required for a cellular proliferation of an organism. The missense mucleic acids required for cellular proliferation of the strains or for endowned an organism or screening for homologous nucleic acids required for a cellular proliferation of an organism are antible and an organism a
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 3339; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                   Malone C,
Carr GJ,
                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-01929228.
08-FEB-2002; 2002US-0072251.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                  (BLIT-) BLITRA PHARM INC.
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Trawick JD,
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Wall D,
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Matches
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RESULT

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(first entry)

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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                Arabidopsis thaliana stress regulated gene SEQ ID NO 3647.
                                                                                                                                                                                                  Arabidopsis thaliana; plant; gene; stress; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harper JF, Kreps J, Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2000; 2000US-027866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-2001; 2001WO-US026685.
                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-304127/34.
                                                                                                                                                                                                                                                                                                                  WO200216655-A2.
                                                                                              21-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2002
                                         ABZ15842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polymucleotide (1) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FKR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ANS64197-AAS94564 represent novel human diagnostic coding sequences. ANS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in the will be printed specification, but was obtained in the will be printed specification.
                                                                                                                                                                                                                                                          Human, chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                               DNA encoding novel human diagnostic protein #18359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 18359; 103pp; English.
                                AAS82555 standard; cDNA; 2182 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217,
23-AUG-2000; 2000US-00649167,
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                                                                                                                                             (first entry)
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Best Local Similarity 100.
Matches 25; Conservative
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P-PSDB; ABG18368.
                                                                                                                                                                                                                                                       Human; chromosome
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                                                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                          13-FEB-2002
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AAS 2555 AAS 8 AAS
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants. Cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thalians stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvalsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    80.8%; Score 20.2; DB 6; Length 2000;
88.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2000 BP; 714 A; 318 C; 295 G; 673 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID MO: 1370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    L.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        975 TTATGICATATATGTTTATGATTTA 951
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Matches
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Gaps

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0; Indels

0; Mismatches

8 g RESULT 7 ABZ15842/c ID ABZ15842 standard; DNA; 2000 BP.

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WPI; 2003-646311/61.
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                       20-NOV-2003
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                                                                                                                                       Query Match
Best Local 9
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                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system discorders, including eye diseases such as retinopathy, neovascular glaucoma an amoular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheijepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                for
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful f
diagnosis and treatment of diseases associated with abnormal cytosine
methylation.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                   Length 5641;
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                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1370; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumour suppressor gene, Lmt intron 3 DNA
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                                                                                    02-JUL-2001; 2001WO-EP007537
                                                                                                        30-JUN-2000; 2000DE-01032529.
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                                                                                                                                                        Piepenbrock C,
                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                           WPI; 2002-130909/17
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                                                WO200200928-A2.
                              Homo sapiens
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                                                                  03-JAN-2002
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Matches
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                                                                                                                                     The invention relates to novel tumour suppressor gene, referred to as Lmt. The invention also relates to the field of cancer therapy and cance diagnostics. The nucleic acid molecule is useful for screening a subject for the presence of an aberration in a gene encoding an LMT. The present sequence is human Lmt intron 3 DNA
                                                                                                                                                                                                                                                                                                                          Other;
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New nucleic acid molecule, useful for screening a subject for the presence of an aberration in a gene encoding an LMT.
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                                                                                                                                                                                                                                                                                                                      Sequence 62782 BP; 15441 A; 9614 C; 9374 G; 14439 T; 0 U; 13914
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                                                                                                                                                                                                                                                                                                                                                                        ch 79.2%; Score 19.3; DB 8; 1 Similarity 91.3%; Pred. No. 1.9e+02; 21; Conservative 0; Mismatches 2;
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Pred. No. 1.9e+02;
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                                                                                   Claim 10; Page 333-358; 373pp; English
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ID AAD58281 standard; DNA; 62782
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Best Local Similarity 91.3%;
Matches 21; Conservative (
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Hybridisation assay, genetic mapping, gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 13710.
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990S-0134370F.
990S-013470P.
990S-0134768P.
990S-0134941F.
990S-0135324F.
                                                                                                                                                                                                                       99US-0121825P.
99US-0123180P.
99US-0125788P.
99US-0125788P.
99US-012648P.
99US-0127462P.
99US-0127462P.
99US-0128234P.
99US-0130845P.
99US-0130845P.
99US-013081P.
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99US-0132484P.
99US-0132485P.
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990S-0132487P.
990S-0132863P.
990S-0134256P.
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990S-0136021P.
990S-0136392P.
990S-01317222P.
990S-0137528P.
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99US-0137724P.
99US-0138094P.
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99US-0138847P.
99US-0139119P.
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99US-0139453P.
99US-0139492P.
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99US-0139458P.
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99US-0139461P.
99US-0139462P.
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                       17-OCT-2000 (first entry)
                                                                                                                         Arabidopsis thaliana
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10-JUN-1999)
14-JUN-1999)
16-JUN-1999)
16-JUN-1999)
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18-UN-1999)
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16-APR-1999;
19-APR-1999;
21-APR-1999;
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28-APR-1999;
30-APR-1999;
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07-JUN-1999;
08-JUN-1999;
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9-MAY-1999
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AAC36413;
 om base 300001 (Human transporter protein encoding LOCUS ADE11169 Accession Ade11169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 226475 BP; 61024 A; 41761 C; 40916 G; 57494 T; 0 U; 25280 Other;
                                                                                                                                                  Gaps
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                                                                                                                       Score 19.8; DB 9; Length 94191;
Pred. No. 1.9e+02;
0; Mismatches 2; Indels 0;
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                                                         110000
210000
310000
ADELLI69 3/C
Continuation (4 of 4) of ADELLI69 from base
WP Sequence split into 4 fragments LOCUS
WP ADELLI69 0
WP ADELLI69 1 100001
WP ADELLI69 2 200001
WP ADELLI69 3 100001
WP ADELLI69 3 100001
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AADS8279 standard; DNA; 226475
                                                                                                                       79.2%;
91.3%;
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                                                                                                       Query Match
Best Local Similarity 91....
Local 21; Conservative
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AAC36413
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AAD58279/c
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9945-0139463P
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9945-0139750P
9945-0139763P
9945-013963P
9945-0140153P
9945-0140153P
9945-01401291P
9945-0140291P
9945-014125P
9945-0141313P
9945-0144313P
9945-014503P
9945-014503P
9945-014503P
9945-014503P
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9945-0147303P
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18 - JUN - 1999

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Length 1293; 990S-0150884P-990S-0151065P-990S-0151065P-990S-0151080P-990S-0151080P-990S-0151080P-990S-0151080P-990S-0151080P-990S-0151080P-990S-015108P-990S-015529P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-015929P-990S-0160980P-990S-0160980P-990S-0160980P-990S-0160980P-990S-0160980P-990S-0161359P-990S-0161359P-990S-0161359P-990S-0161359P-990S-0161359P-990S-0161359P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990S-0161350P-990 99US-0161992P. 99US-0161993P. 99US-0162142P. 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 32-SEP-1999; 32-SEP-1999; 32-SEP-1999; 32-SEP-1999; 32-SEP-1999; 32-SEP-1999; 33-SEP-1999; 34-OCT-1999; 34-OCT-1999; 34-OCT-1999; 34-OCT-1999; 35-OCT-1999; 35-OCT-1999; 36-OCT-1999; 

3. 3. Score 19.2; DB 3 Pred. No. 3e+02; 0; Mismatches 24 TTAAGTCATATATGTTTTTGACTT Query Match 76.8%; Best Local Similarity 87.5%; Matches 21; Conservative

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610000 364 TTAAGTCTTATATGTTGATGACTT 387 ABA92787 fr fragments Begin 100001 200001 300001 400001 500001 ABA92787\_2/c
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Continuation (3 of 7) of AB
WP Sequence split into 7 fr.
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WP ABA92787\_1
WP ABA92787\_2
WP ABA92787\_3
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                                                                                                                                                                        Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; fimumuosuppressive; antihiflammatory; anti-HIV; antibacterial; vulnerary; antiparakinsonian; antisickling; antianaemic; antiarthritic; cancer; antifheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antididabetic; antiulcer; anticonvulsant; antibungal; antiparasitic; cardiant; immue discreber; cardiovascular discreber; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
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               Score 18.8; DB 6; Length 110000;
Pred. No. 4.6e+02;
0; Mismatches 2; Indels 0;
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                                                          23338 AAATCATATTTTTTTGACTT 23317
640681
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2000US-0228924P
                                                                                                                                                                                                                                                                                            17-JAN-2001; 2001WO-US001334
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Matches 20, Conservative
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Query Match 74.4%; Score 18.6; DB 5; Length 561; Best Local Similarity 84.0%; Pred. No. 5.1e+02; Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps

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1 TTAAGTCATATATGTTTTTGACTTA 25

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Search completed: May 26, 2004, 17:50:16 Job time : 182.526 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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May 26, 2004, 16:18:00 ; Search time 39.8504 Seconds (without alignments) 348.146 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-10-676-299-9 25 1 ttaagtcatatatgtttttgactta 25 Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 seqs, 277475446 residues Searched:

Total number of hits satisfying chosen parameters:

1365418

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	Description	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Sequence	Sequence		Sequence			Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
OFFICE	ID	US-09-790-988-1	US-09-461-325-73	US-10-012-542-73	US-10-204-708-1	US-09-497-855A-37	US-09-497-855A-44	US-09-601-198-111	US-09-328-352-1849	US-08-356-354-5	US-08-778-656-5	US-09-976-594-68	US-09-453-702B-60	US-09-495-050A-43	US-09-328-352-1986	US-08-904-263A-3	US-09-434-123A-3	US-08-851-567B-48	US-08-851-567B-46	US-09-637-048C-1	US-09-817-514A-1	US-09-616-289-51	US-09-790-988-1	US-09-134-000C-3252	US-09-328-352-149	US-09-328-352-2210	US-09-328-352-188	US-09-324-803C-13
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Sequence 11, Appl Sequence 12, Appl Sequence 11, Appl Sequence 130, Appl Sequence 1, Appl Sequence 1, Appl Sequence 29, Appl Sequence 51, Appl Sequence 443, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 38, Appl Sequence 38, Appl Sequence 38, Appli
US-09-324-803C-21 US-09-324-803C-12 US-09-324-803C-12 US-09-328-352-370 US-09-328-352-370 US-09-328-352-346 US-08-956-171E-344 US-08-956-171E-443 US-08-956-171E-443 US-08-956-171E-443 US-08-311-490-1 US-08-311-490-1 US-08-311-30-1 US-09-511-477-38 US-09-511-477-38 US-09-511-477-38
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Gaps
                                     Us-09-790-988

| Patent No. 6632935
| GRREAL INFORMATION
| APPLICANT: SHIGENOBU, SHUJI
| APPLICANT: SHIGENOBU, SHUJI
| APPLICANT: WATANABE, HIDEMI
| APPLICANT: HATTONI, WASAHIRA
| APPLICANT: HATTONI, WASAHIRA
| APPLICANT: SAKAKI, VOSHIYUKI
| TITLE OF INVENTION: GENCME DNA OF BACTERIAL SYMBIONT OF APHIDS
| FILE REFERENCE: 0801366/0159
| FILE REFERENCE: 0801366/0159
| CURRENT PILING DATE: 2001-02-23
| FRIOR PILIATION NUMBER: US/09/790,988
| CURRENT PILING DATE: 2001-04-07
| WUMBER OF SEQ ID NOS: 7
| SOFTWARE: PatentIn Ver. 2.1
| LENGTH: 640681
| TIPLE ON ARCHITER OR SEG ID NOS: 7
| CORGANISM: Buchnera SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
75.2%; Score 18.8; DB 4; Length 640681;
Best Local Similarity 90.9%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 2; Indels 0;
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RESULT 2
US-09-461-325-73/C

Sequence 73, Application US/09461325A

Patent No. 6475/53

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1
CURRENT APPLICATION NUMBER: US/09/461,325A

CURRENT FILING DATE: 1999-12-14

SARLIER APPLICATION NUMBER: PCT/US99/13418

RARLIER PLING DATE: 1999-06-15

RARLIER PLING DATE: 1998-06-16

RARLIER PLING DATE: 1998-06-16

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| Retent No. 667731
| GENERAL INFORMATION:
| APPLICANT: OLEX, Alexander | APPLICANT: PIERPENBROCK, Christian | APPLICANT: SERLIN, Kurt | APPLICANT: SERLIN, Kurt | APPLICANT: SERLIN, Kurt | APPLICANT: STRIN, Kurt | APPLICANT: STRIN, Kurt | APPLICANT | APPLICA
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| Patent No. 6627741
| Sexuence No. 6627741
| Sexuence No. 6627741
| Sexuence No. 6627741
| Sexuence No. 6627741
| Patence No. 6627741
| APPLICANT: Ruben et al.
| TITLE OF INVENTION: 94 Human Secreted Proteins
| FILE REPRENCE: P200291
| CURRENT APPLICATION NUMBER: US/10/012,542
| CURRENT FILING DATE: EARLIER FILING DATE: 1999-12-14
| PRIOR PILING DATE: EARLIER FILING DATE: 1999-16-16
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
| PRIOR PILING DATE: EARLIER PILING DATE: 1998-06-22
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| FARLIER FILING DATE: 1998-06-16 |
| EARLIER APPLICATION NUMBER: 60/090,112 |
| FARLIER FILING DATE: 1998-06-22 |
| FARLIER PEPLICATION NUMBER: 60/090,113 |
| FARLIER PEPLICATION NUMBER: 60/090,113 |
| FARLIER PEPLICATION NUMBER: 60/090,113 |
| FARLIER PER PER DATE: 1998-06-22 |
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| TYPE: DNA |
| OKGAMISM: Homo sapiens |
| US-09-461-325-73 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 73, Application US/10012542
Patent No. 6627741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.8%;
Best Local Similarity 87.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTAAGTCATATATGTTT
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PORGANISM: Homo sapiens
US-10-012-542-73
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US-10-204-708-1
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RESULT 5

US-09-497-855A-37

US-09-497-855A-37

Sequence 37, Application US/09497855A

Patent No. 6605432

GENERAL INFORMATION:

PAPLICANT: Huang, Tim

TILE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION

FILE REFRENCE: UMOBER: US/09/497,855A

CURRENT APPLICATION NUMBER: 06/120,592

PRIOR PELING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-05

NUMBER: OF SEQ ID NOS: 54

SOFTWARE: Patentin Version 3.0

SEQ ID NOS: 54
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US-09-497-855A-44
US-09-497-855A-44
Sequence 44, Application US/09497855A
Sequence 42, Application US/09497855A
GENERAL INFORMATION:
APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REPREBRENCE: UNC15.23
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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71.2%; Score 17.8; DB 4; Length 193303;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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by Assessing DNA Methylation
           TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILID DATE: 2003-05-06
FRIOR PILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: BE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-31
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TAAGTCATATATGTTT
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CORGANISM: Homo sapiens;
US-09-497-855A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193303
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Gaps

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WG-08-356-354-5/c

Sequence 5, Application US/08356354

Sequence 5, Application US/08356354

Patent No. 5767364

GERERAL INFORMATION:

APPLICANT: SONNEWALD, Uwe

TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: Ostrolenk, Paber, Gerb & Soffen

STREET: 1180 Avenue of the Americas

CITY: New York

STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.8%; Score 17.2; DB 1; Length 2930; Best Local Similarity 86.4%; Pred. No. 2.5e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0;
                               Score 17.2; DB 4; Length 1053; Pred. No. 2.5e+02; 0; Mismatches 3; Indels 0
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COUNTRY BEADALE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READALE Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
FILING DATE: 20-DEC-1994
FILING DATE: 20-DEC-1994
FILING DATE: 22-UN-1993
PRIOR APPLICATION NUMBER: US PCT/EP93/01605
FILING DATE: 22-UN-1993
PRIOR APPLICATION NUMBER: DE P42 20 758.4
FILING DATE: 24-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meliman, Edward A.
REGISTRATION NUMBER: 24,735
REPERENCE/DOCKET NUMBER: P/951-105
FELEPHONE: (212) 382-0700
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEFAX: (212) 382-0888
TELESTA: 2336925
SEQUENCE CHARACTERISTICS:
ELENGTH: DAGE PAITE
TUDES TO THE PATENTING TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2885 rragcricararaggrirritaac 2864
                                                                                                                                                                                                                                                                                   119 AAACCATATGTGTTTTTGACTT 140
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                                        Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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STRANDEDNESS: sing
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ORIGINAL SOURCE:
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APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Hainer, Cheryl R.
APPLICANT: Last Contract and Last Contract Contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FLING DATE: 1999-02-18
PRIOR PELING DATE: 1999-02-05
PRIOR PILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
SEQ ID NO 44
LENGTH: 193303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 TTGAGTCACATATGATTTTGAATT 46
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-1849
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                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-44
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Gaps

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APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkert, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.8%; Score 17.2; DB 4; Length 5982; 86.4%; Pred. No. 2.5e+02; ive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: WITH PC COMPATIBLE SOFTWARE: WORD PErfect 8.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Dec-1999
CLASSIFICATION DATA:
APPLICATION INFORMATION:
                                                                                                                                                                                                                                                                      PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 978439.4
NAME/KEY: unsure
LOCATION: 1627
OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 231-5000
TELEFAX: (608) 251-9166
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PELICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 68
LENGTH: 5982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4795 AAGGCATATAAGTTTTTGACCT 4774
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MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.4<sup>5</sup>
warches 19; Conservative
                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-453-702B-60
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US-09-976-594-68/C
Sequence 68, Application US/09976594
; Sequence 80. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
                                                                                                GENERAL INFORMATION:

APPLICANT: SONDEWALD, UWE

APPLICANT: SONDEWALD, UWE

TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
WITHER FOF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ostrolenk, Paber, Gerb & Soffen

STREET: 1180 Avenue of the Americas

CITY: New York

STATE: New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . LOCATION: 118.:2841
. OTHER INFORMATION: /note= "Sucrose-Phospahte-Synthase"
US-08-778-656-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                    STATE: NY
COUNTRY: UNY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APPLICATION DATA:
SUSTWARE: PACENTIN Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/778,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

68.8%; Score 17.2; DB 2;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,354
PILING DATE: 20-DEC-1994
APPLICATION NUMBER: US PCT/EP93/01605
FILING DATE: 22-UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P42 20 758.4
PILING DATE: 24-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mellman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET UNBER: P/951-105
TELECOMMUNICATION INFORMATION:
TELEPRA: (212) 382-0700
TELEFAX: (212) 382-0888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2885 Traccicararaceritricae 2864
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       RESULT 10
US-08-778-656-5/c
'Sequence 5, Application US/08778656
'Patent No. 5976869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Solarum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 236925
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2930 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
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18-9-94-254-376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 TTTAGTCATATTTGTGTTTAACGTA 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAMB/KGY: CDS
; LOCATION: 70.3762
US-08-904-263A-3
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         RESULT 15
US-08-904-263A-3/c
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i Sequence 43, Application US/09495050A

j Sequence 43, Application US/09495050A

j Remer No. 6492505

general No. 6492505

j General No. 6492505

j APPLICANT: Guegler, Rarl, J.

APPLICANT: Guegler, Rarl, J.

APPLICANT: Guegler, Rarl, J.

APPLICANT: A-Young, Uanice

TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F

TITLE OF INVENTION: US/09/495, 050A

CURRENT APPLICATION NUMBER: US/09/495, 050A

CURRENT FILING DATE: PA0013 US/09/495, 050A

RELOR FILING DATE: February 1, 1999

NUMBER OF SEQ ID NOS: 305

SEQ ID NO 43

LENGTH: 449
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Sequence 1986, Application US/09328352
Patent No. 6562958
GRNERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC AID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTOS9-0299.
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1986
LENGTH: 927
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                                                                                                   Length 49795;
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Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.0%; Score 17; DB 4; Length 927; 80.0%; Pred. No. 3e+02;
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                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6492505 948051CB1
                                                                                                   Query Match 68.8%; Score 17.2; DB 4; Best Local Similarity 86.4%; Pred. No. 2.5e+02; Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-453-7028-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TTAAGTCATATATGTTTTTGACTTA 25
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                                                                                                                                                                                                                                                                                       42082 rahricaradarcrirriracr 42103
                                                                                                                                                                                                                              2 TAAGTCATATATGTTTTTGACT 23
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US-09-328-352-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.03
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-328-352-1986/c
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Gaps ő

5; Indels

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Sequence 73, Application US/09461325A
Patent No. 6475753
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 94 FUMAN Secreted Proteins
FILE REFERENCE: P2029P1
CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
FARLIER APPLICATION NUMBER: PCT/US99/13418
FARLIER APPLICATION NUMBER: 60/089,507
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER FILING DATE: 1998-06-16
FARLIER FILING DATE: 1998-06-16
FARLIER RPLING DATE: 1998-06-16
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Best Local Similarity 90.9
Matches 20; Conservative
520
551
559
669
721
721
103
1103
1166
5311
6314
6314
8855
8855
29793
29793
83450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
GRGANISM: Buchnera sp.
US-09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 640681
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US-09-461-325-73
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Sequence 17, Appl
Sequence 111, App
Sequence 1849, Ap
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 60, Appli
Sequence 60, Appli
Sequence 60, Appli
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3, Appli
3, Appli
46, Appl
1, Appli
1, Appli
51, Appli
325, Appli
149, Appli
149, Appli
149, Appli
1210, 
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Sequence 73, Appl
Sequence 73, Appl
                                                                                                                                                                  May 26, 2004, 16:18:00 ; Search time 39.8504 Seconds (without alignments) 348.146 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents NA:*

1. /cgr2_6/ptodaxca/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodaxca/2/ina/6B_COMB.seq:*

3. /cgn2_6/ptodaxca/2/ina/6A_COMB.seq:*

4. /cgn2_6/ptodaxca/2/ina/6B_COMB.seq:*

5. /cgn2_6/ptodaxca/2/ina/PCTUS_COMB.seq:*

5. /cgn2_6/ptodaxca/2/ina/PcTUS_COMB.seq:*

6: /cgn2_6/ptodaxca/2/ina/PcTUS_COMB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-461-325-73

US-10-204-708-1

US-09-497-855A-37

US-09-497-855A-44

US-09-601-198-1111

US-09-328-352-1849

US-09-376-594-68

US-09-976-594-68

US-09-976-986-1

US-09-328-352-149

US-09-134-000C-3252

US-09-328-352-149

US-09-328-352-149

US-09-328-352-149

US-09-328-352-149

US-09-328-352-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                     682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                 US-10-676-299-10
25
1 taagtcaaaacatatatgacttaa 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                             IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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72.8 1486

72.8 10467

71.2 193303

70.4 193303

70.4 2930

68.8 1053

68.8 2930

68.8 2930

68.8 45982

68.0 3825

68.0 3825

68.0 3825

68.0 7551

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                                                                                                                                                                                                                                                                                                                    Sequence:
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                                                                                                                                                                       Run on:
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US-09-324-803C-21
US-09-324-803C-11
US-09-324-803C-11
US-09-324-803C-11
US-09-328-352-370
US-09-328-352-3485
US-09-482-23-51
US-08-956-171E-344
US-08-956-171E-443
US-08-956-171E-443
US-08-956-171E-344
US-08-956-171E-344
US-08-322-760A-1
US-08-322-760A-1
US-09-312-38
US-09-311-37-38
US-09-511-477-38
US-09-511-477-38
US-09-511-477-38
US-09-511-477-38
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                                                                                                                                                                                                                   ALIGNMENTS
ALIGNMENTS
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OF INVENTION: by Assessing DNA Methylation
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Patent No. 6677731
Patent No. 6677731
Patent No. 225.
APPLICANT: OLEK, Alexander
APPLICANT: PIEPERMROCK, Christian
APPLICANT: BERLIN Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REPERENCE: PZO291
CURRENT APPLICATION NUMBER: US/10/012,542
CURRENT FILING DATS: 2001-12-12
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
FRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
FRIOR FILING DATE: EARLIER FILING DATE: 1990-06-16
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
FRIOR FILING DATE: EARLIER FILING DATE: 1990-06-16
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
FRIOR FILING DATE: EARLIER FILING DATE: 1990-06-16
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
FRIOR FILING DATE: EARLIER FILING DATE: 1990-06-12
FRIOR FILING DATE: EARLIER FILING DATE: 1990-06-22
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EARLIER APPLICATION NUMBER: 60/089,510
FEARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER FILING DATE: 1998-06-22
FEARLIER PEPPLICATION NUMBER: 60/090,113
EARLIER PILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 73
LENGTH: 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 AGTCAAAAGAGATATGACTTTA 468
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Matches 20; Conservative
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US-10-012-542-73
                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-325-73
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US-10-204-708-1/c
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LENGTH: 1486
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US-10-012-542-73
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APPLICANT: Hoang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILLE REFERENCE: UNDOIS23
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-497-855A-44/c
US-09-497-855A-44/c
| Sequence 44, Application US/09497855A
| SEXEMAL INFORMATION:
| APPLICANT: Huang, Tim
| TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
| FILE REPERENCE: UNC12.3
| CURRENT APPLICATION UMBER: US/09/497,855A
| CURRENT FILING DATE: 2000-02-04
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; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-1
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72.8%; Score 18.2; DB 4; Length 10467;
Best Local Similarity 87.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0;
TITLE OF INVENTION:
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PLING DATE: 2000-04-06
PRIOR PLING DATE: 2000-04-06
PRIOR PLING DATE: 2000-04-06
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-06
PRIOR PLING DATE: 2000-04-06
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
LENTH: 10467
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; Sequence 37, Application US/09497855A

; Patent No. 6605432

; GRNERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Homo sapiens;
US-09-497-855A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193303
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APPLICANT: SONNEWALD, UWE
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
NUMBER OF SEQUENCES:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                  Query Match 68.8%; Score 17.2; DB 4; Length 1053; Best Local Similarity 86.4%; Pred. No. 2.5e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 118..2841
OTHER INFORMATION: /note= "Sucrose-Phospahte-Synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NS
CUDNING: NS
CUDNING: US
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,354
FILING DATE: 20-DEC-1994
CLASSIFICATION NUMBER: US/08/356,354
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/356,354
FILING DATE: 22-JUN-1993
FILING APPLICATION DATA:
APPLICATION NUMBER: 24-JUN-1992
ATPLICATION NUMBER: 24-JUN-1992
ATPLICATION NUMBER: 24,735
REGISTRATION NUMBER: 24,735
TELEPRAK: (212) 382-0700
TELEPRAK: (212) 382-0700
TELEPRAK: (212) 382-0700
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                                                                                                                                                                 140 AAGTCAAAACACATATGGTTT 119
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                                                                                                                  2 AAGTCAAAACATATATGACTT 23
                                                                                                                                                                                                                                                                 US-08-356-354-5; Sequence 5, Application US/08356354; Patent No. 5767365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 236925
INFORMATION POR SEQ ID NO: 5
SEQUENTICE CHARACTERISTICS:
LENGTH: 2930 base pairs
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MOLECULE TYPE: C
ORIGINAL SOURCE:
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US-09-328-352-1849/C
; Sequence 1849, Application US/09328352
; Patent No. 6563958
; GENERAL INFORMATION:
; APPLICANT GATY L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII POR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: BAUMANNII POR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC39-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1849
. LENGTH: 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Cassell, Gail H.

APPLICANT: Cassell, Gail H.

APPLICANT: Cassell, Gail H.

APPLICANT: Class, Jennifer S.

APPLICANT: Glass, John I.

APPLICANT: Heiner, Cherryl R.

APPLICANT: Holmer, Bliot

TITLE OF INVENTION: UNCABLY ACID PROBES AND METHOD FOR DETECTING URRAPLASNA

TITLE OF INVENTION: UNCABLY LOGONOMY

TITLE OF INVENTION: UNCABLY LOGONOMY

CURRENT FILING DATE: 2000-12-08

PRIOR APPLICATION NUMBER: 60/073,189

PRIOR PLILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 181

SOFTWARE PARENTED ACID NOS: 181

SOFTWARE PARENTED ACID NOS: 181

SEQ ID NO 111

LENGTH: 711
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                                                                                                                                                                                                                                                                                              Length 193303;
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                              Query Match

71.2%; Score 17.8; DB 4;
Best Local Similarity 90.5%; Pred. No. 1.46+02;
Matches 19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/118,760
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AAGTCAAAACATATATGACTTAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                37190 Grcaaaracarararargccrra 37170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 111, Application US/09601198 Patent No. 6531583
                                                                                                                                                                                                                                                                                                                                                                                              4 GTCAAAACATATATGACTTA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Ureaplasma urealyticum
US-09-601-198-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens;
US-09-497-855A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-601-198-111
                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WAGASON
STATE: WAGASON

COUNTRY: US

COUNTRY: US

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OWENTY SYTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
PILING DATE: 03-Dec-1999
CLASSIFICATION NUMBER: 06/110,955
PRIOR APPLICATION NUMBER: 60/110,955
PRIOR APPLICATION NUMBER: 5.3366
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET 1098
ATTORNEY/AGENT INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATENSTICS:
TELEFAX: (608) 251-5000
TELEFAX: (608) 251-5000
TELEFAX: (608) 251-5000
TELEFAX: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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OTHER INFORMATION: Incyte ID No. 6673549 978439.4

NAME/KEY: unsure

LOCATION: 1627

US-09-976-594-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.8%; Score 17.2; DB 4; Best Local Similarity 86.4%; Pred. No. 2.5e+02; Matches 19; Conservative 0; Mismatches 3;
FILE REPERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILIGA DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
LENGTH: 5992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4774 AGGICAAAACTTATATGCCTT 4795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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US-09-453-702B-60/c
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Patent No. 6673549
GENERAL INPORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
                                                                                                             GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SONNEWALD, UWE

TITLE OF INVENTION: BNA SEQUENCES AND PLASMIDS FOR THE

TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION

NUMBER OF SEQUENCES:

ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen

STRERT: 1180 Avenue of the Americas

CITY: New York

STATE: NY

CONNTRY: US
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GTHER INFORMATION: /note= "Sucrose-Phospahte-Synthase"
US-08-778-656-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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CUDNIKK: U.S.
CUDNIKK: U.S.
CUDNIKK: D.S.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,656
FILING DATE: 20-DEC-1994
APPLICATION NUMBER: US PCT/EP93/01605
FILING DATE: 22-JUN-1993
PRIOR APPLICATION NUMBER: B PCT/EP93/01605
FILING DATE: 22-JUN-1993
PRIOR APPLICATION NUMBER: B P42 20 758.4
FILING DATE: 24-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P42 X0 758.4
FILING DATE: 24-JUN-1992
ATTORNEY/AGENT INFORMATION:
ANALYMENT OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.8%; Score 17.2; DB 2; Best Local Similarity 86.4%; Pred. No. 2.5e+02; Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24,735
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKST NUMBER: P/951-105
TELEPHONE: (212) 382-0700
TELEPHONE: (212) 382-0700
TELERY: (212) 382-0888
TELEX: 256925
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 2930 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2864 Grcadadaccrarardagcraa 2885
                                                                      Sequence 5, Application US/08778656
Patent No. 5976869
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ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
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NAME/KEY: CDS
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US-09-976-594-68
          RESULT 10
US-08-778-656-5
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GENERAL INTORNATION: G015889

GENERAL INTORNATION: GUNNAR
APPLICANT: LINDAHL, GUNNAR
APPLICANT: STALHAMMAR-CARLEMALM,
APPLICANT: STALHAMMAR-CARLEMALM,
APPLICANT: STALHAMMAR-CARLEMALM,
APPLICANT: STALHAMMAR-CARLEMALM,
APPLICANT: STALHAMMAR-CARLEMALM,
APPLICANT: STARMERGH
APPLICANT: STARMERGH
APPLICANT: STARMERGH
APPLICANT: STARMERGH
APPLICANT: STARMERGH
APPLICANT: STARMERGH
APPLICANT: STALMERGH
APPLICANT: 
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COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,263A
PILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INPORMATION:
NAME: SYENSSON, LECHARD R
REGISTRATION NUMBER: 30,330
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                                                      US-08-904-263A-3; Sequence 3, Application US/08904263A; Patent No. 6015889
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TELECOMUNICATION INFORMATION: TELECHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 3825 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
70..3762
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US-08-904-263A-3
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US-09-495-050A-43
US-09-495-050A-43
US-09-495-050A-43
US-09-495-050A-43
Fatence 43, Application US/09495050A
Fatence 43, Application US/09495050A
Fatence 43, Application US/09495050A
Fatence 43, Application US
Fatence 43, Application US
Fatence 43, Application US
Fatence 44, Application US
Fatence 44, Application US
Fatence 45, Application US
Fatence 75, Vanua, Janice
Fatence 77, Vanua, Janice
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Sequence 1966, Application US/09328352

GENERAL INFORMATION:

APPLICANT GATY L. Breton et al.

APPLICANT GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US/09-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 1986

LENGTH: 927
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                                                                                                                                           Match 68.8%; Score 17.2; DB 4; Length 49795; Local Similarity 86.4%; Pred. No. 2.5e+02; les 19; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 948051CB1
US-09-495-050A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.0%; Score 17; DB 4;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches
         ; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-453-702B-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TAGCCAAAACATATGACTTAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                   42103 AGTAAAAACATCTATGAATTA 42082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAAGTCAAAACATATATGACTTAA 25
                                                                                                                                                                                                                                                                                                                                         3 AGTCAAAACATATATGACTTA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-328-352-1986
                                                                                                                                                     Query Match
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## ALIGNMENTS

RESULT 1

ArsR; arsenic resistance operon; biosensor; ss; arsenic. E. coli Arsk binding oligonucleotide PLASSIB. BP. 15-AUG-2002; 2002US-00222952. 20-AUG-2001; 2001US-0313714P. ACD28589 standard; DNA; 21 (first entry) WPI; 2003-576876/54. (LAIN/) LAING L G. Escherichia coli. US2003096275-A1. 22-MAY-2003. 10-OCT-2003 Laing LG; ACD28589; ACD28589 

New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 35; Page 15; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein biosensor device for detecting the presence of the analyte. Also included are biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample, and the areance resistance operon of E. coil) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1970 of the ArsR sequence appearing as ABUG3440 binding to a nucleic acid

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Mismatches

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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of
sequence comprising oligonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the bottom strand of an oligonucleotide which binds tto a plasmid expressed Arsk protein and is used in the biosensor of the invention
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presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte: (2) an isolated nucleic acid containing a specifically binds the analyte: (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein cto the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of the analyte. Also included are a compared to the arsenic resistence operno of R. coli) protein comprising an part of the arsenic resistence operno of R. coli) protein comprising an amino acid sequence appearing as ABUG3440 binding to a nucleic acid sequence comprising oligonucleotides appearing as ACD28584.ACD28591. The system is useful for detecting the presence of analyte in a sample. The present is equence is the bottom strand of an oligonucleotide which binds to a plasmid expressed Arsk protein and is used in the biosensor of the invention
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    coli Arsk binding oligonucleotide PLASLIB.

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presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated mucleic acid containing a specifically binds the analyte; (2) an isolated mucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, and an area of the area of the area of the area of the analyte in a sample, and an Arsk (encoded by part of the areanic resistance operon of E. coll) protein comprising an amino acid sequence appearing as least 90% identical to amino acids 1-97 of the Arsk sequence appearing as ABU6340 binding to a nucleic acid system is useful for detecting the presence of analyte in a sample. The present sequence is the top strand of an oligomucleotide which binds to a plasmid expressed Arsk protein and is used in the biosensor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of
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                                                                                             E. coli ArsR binding oligonucleotide PLASLIT
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                                                                                                                                                                                                                                                                                                                                  ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABB77960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infections. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                             Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Begin
                                                                                                                                                                                                                    WPI; 2002-381255/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (13 of 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. Sequence split into
Fragment Name
AAT42063 00
AAT42063 02
AAT42063 02
AAT42063 03
AAT42063 04
                                                                                                                                                                                                                                    P-PSDB; ABP39987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT42063_05
AAT42063_06
AAT42063_07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT42063 14
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AAT42063_0
                          JS6380370-B1
                                                                                   13-AUG-1998;
                                                                                                                 14-AUG-1997;
                                                                                                                             08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT42063
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                                                        30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT42063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Continuation
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detecting the

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100.0%; Score 21; DB 8; Length 30; 100.0%; Pred. No. 4.9; ive 0; Mismatches 0; Indels

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23 TAACCAAAAACGCATATGATT 1 TAACCAAAAACGCATATGATT

(first entry)

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Gaps

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Indels

Score 17.8; DB 2; Pred. No. 1.6e+02; 0; Mismatches 2;

84.8%; 90.5%;

Query Match Best Local Similarity 90.5 Matches 19; Conservative

Length 110000;

ADA53054 RESULT

8

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The specification describes a nucleic acid construct for transforming a plant cell. The construct comprises a promoter which is selectively cativated in cells of propagating material for a plant, operatively linked to a nucleotide sequence whose transcription leads to an alteration in the levels of polyamines produced in the transformed cells. The construct is useful for altering the levels of polyamines in a construct is useful for altering the levels of polyamines in a propagating material for a cultivated plant. Transgenic plants comprising the construct are useful in foodstuffs, pharmaceutical preparations, the construct are useful in foodstuffs, pharmaceutical preparations of the construct are useful in foodstuffs, pharmaceutical preparations, carrived from these plants are useful for the manufacture of a medicament of or use in the treatment or prophylaxis of hyperproliferative diseases, constructivally concer, Modgkin's disease, porlass, ulcerative diseases, irritable bowel syndrome and diamine/polyamine oxidase deficiency, normal construction, or prophylaxis of the lung or gut and for supporting growth in babies and young children, human immunodeficiency virus (HIV).

The created infection, and in other patients suffering from post-surgiacal creament constructs and transfusion induced suppression. The present sequence represents a high molecular weight constructs of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid construct for transforming a plant cell, comprises a selectively activated promoter, operatively linked to a nucleotide sequence whose transcription leads to altered polyamine levels.
       Promoter; polyamine; transgenic plant; foodstuff; cancer; trauma; nutritional formulation, hyperproliferative disease; Hodgkin's disease; psoriasis; ulcerative colitis; irritable bowel syndrome; healing; post-operational recovery; liver regeneration; kidney hypertrophy; sepsis; transfusion; laminin box; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 16.8; DB 4; Length 1257; 90.0%; Pred. No. 4.18+02; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1257 BP; 403 A; 261 C; 237 G; 356 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comamonas testosteroni NI 1 amidase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 39; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                               NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ67726 standard; DNA; 1491 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sarcelo-Ensesa P, Tiburcio AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AACTAAAACACATATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AACCAAAAACGCATATGATT
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(first entry)
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les 18; Conservative
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(DUPO ) DUPONT UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-182965/18.
                                                                                                                                                        Triticum aestivum.
                                                                                                                                                                                                   40200109358-A1
                                                                                                                                                                                                                                                                                                                                      30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2003
25-MAR-2003
16-MAR-1995
                                                                                                                                                                                                                                               08-FEB-2001
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BXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                              Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of a high molecular weight prolaminin promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel human secretory or membrane proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-ADAS4071). The coding sequences are useful in the gene therapy of diseases caused by abormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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Local Similarity 94.7%; Pred. No. 2.3e+02;
les 18; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3727 BP; 927 A; 839 C; 1016 G; 945 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 622; 205pp; English.
                                                                      38891 TAACCAAAAACGCATATTGTT 38911
                                                                                                                                                                                                                                                                                                                       Human coding sequence, SEQ ID 622.
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                             21
                                                                                                                                                                                  ADAS3054 standard; cDNA; 3727 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.
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                          TAACCAAAAACGCATATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002; 2002EP-00006586.
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                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-395539/38.
P-PSDB; ADAS4693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1293569-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                              20-NOV-2003
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                                                                                                                                                                                                                                   ADA53054;
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AAF54914/c

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RESULT 8

Best Loc Matches

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The amidase gene was isolated from a Comamonas testosteroni genomic DNA library using a degenerate probe based on the N-terminal amino acid sequence of the purified enzyme. The amidase is able to hydrolyse amides to carboxylates and has higher activity on ammonium adipmate than on adipamide. The enzyme is particularly useful for converting ammonium adipamete to diammonium adipate for production of nylon 6,6 or for converting 5-cyanovaleramide to 5-cyanovalerate (an intermediate for caprolactam used to make nylon-6). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic; antianzericsclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiatitic; antidiabetic; antisoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                         New amidase with greater activity on adipamate than on adipamide - a related DNA and microorganisms producing it, partic used to produce ammonium adipate or 5-cyanovalerate for nylon mfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.8; DB 2; Length 1491;
Pred. No. 4.18+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1491 BP; 546 A; 239 C; 262 G; 444 T; 0 U; 0 Other;
              amidase; ammonium adipamate; diammonium adipate; nylon 6.6; 5-cyanovaleramide; 5-cyanovalerate; caprolactam; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune system associated gene SEQ ID NO: 228.
                                                                                                                                                                                                                                                                                                                                                             Le Cog A, Levyschil S,
                                                                                               Location/Qualifiers
127. .1383
/*tag= a
/product= "amidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1031 TAACCAAAGACGAATATGAT 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL32255 standard; DNA; 18154 BP
                                                                  Comamonas testosteroni; NI 1.
                                                                                                                                                                                                                                                          94WO-FR000080.
                                                                                                                                                                                                                                                                                         93FR-00001062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 80.0%;
Local Similarity 90.0%;
Les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 2; 55pp; French
                                                                                                                                                                                                                                                                                                                            RHON ) RHONE POULENC CHIM
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P-PSDB; AAR60155.
                                                                                                                                                                                                                                                                                                                                                             Cerbeland E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                            21-JAN-1994;
                                                                                                                                                                                                                                                                                             27-JAN-1993;
                                                                                                                                                                                         WO9417190-A1
                                                                                                                                                                                                                          04-AUG-1994
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Best Local S:
Matches 18
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Soubrier F;

Petre D,

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid theuxemia, Alzheimer's disease, AlDs, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic library for identifying diagnostic and therapeutic compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful f
diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18154 BP; 6013 A; 112 C; 3588 G; 8441 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 16.8; DB 6; Length 18154; 90.0%; Pred. No. 4.3e+02; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 228; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
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                                                                                                                                                                                 Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-2000; 2000WO-US016649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0140121P.
                                                                                 02-JUL-2001; 2001WO-EP007537.
                                                                                                          30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patterson C,
                                                                                                                                                                               Piepenbrock C,
                                                                                                                                                      (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic fragment #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-041427/05
                                                                                                                                                                                                          WPI; 2002-130909/17
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                            W0200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1999;
Homo sapiens.
                                                                                                                                                                                                                                                                   methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-2000
                                                      03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF28554;
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AAF28554
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                                                                 The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF2854). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinustiis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                   Sequence 269223 BP; 77067 A; 56596 C; 57380 G; 78180 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           Gaps
and for identifying virulence factors, regulatory elements and drug
targets, comprises Moraxella catarrhalis nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                               Length 269223;
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                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human map-related biallelic marker SEQ ID NO:2280
                                                                                                                                                                                                                                                            Score 16.8; DB 4;
Pred. No. 4.5e+02;
0; Mismatches 2;
                                           Claim 1; Page 486-545; 545pp; English.
                                                                                                                                                                                                                                                                                                                                          142064 AGCCAAAAACGCATATCATT 142083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 717; 2745pp; English.
                                                                                                                                                                                                                                                                                                                         21
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                                                                                                                                                                                                                                                             Match 80.0%;
Local Similarity 90.0%;
les 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {first entry}
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                                                                                                                                                                                                        and meningitis
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23-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variation
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                                                                                                                                                                                                                                                                Query Match
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AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at postition 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention

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The present invention describes a composition (1) comprising: carriers and immunostimulants; and a polypeptide (11) of a ovarian tumour perspective encoded by a polynucleotide (111) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (1) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contexting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian
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have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential effications responses to and side effects from the differential effications responses to and side effects from the N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing
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                                                                                                                                                                                                                                                                                 77.1%; Score 16.2; DB 3; Length 47; 85.7%; Pred. No. 7.38+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian cancer related cDNA clone SEQ ID NO:10855.
                                                                                                                                                                                                                                                   Sequence 47 BP; 13 A; 3 C; 8 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 10855; 489pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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ABL87877 standard; cDNA; 343
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Nes 18; Conserv
                                                                                                                                                                                                              present invention
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Matches
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tumour protein comprising contacting T cells with (III) or (III). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate ceils and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                          Length 343;
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                                                                                                        Sequence 343 BP; 117 A; 52 C; 50 G; 124 T; 0 U; 0 Other;
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                                                                                                                                        77.1%; Score 16.2; DB 6;
llarity 85.7%; Pred. No. 7.5e+02;
Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate expression marker cDNA 31684.
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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Best Local Similarity
Matches 18; Conserv
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18-JUL-2000;
13-DEC-2000;
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                   Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, 8s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                 Gaps
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                                 Indels
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Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                      Human prostate expression marker cDNA 40652
                                 0; Mismatches
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                Best Local Similarity 85.74
Matches 18; Conservative
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Les 18; Conserv
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Search completed: May 26, 2004, 17:50:12

Length 352;

DB 5;

Score 16.2;

77.18;

Query Match

Job time : 151.962 secs

Thu May 27 10:11:47 2004

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